

94073

## STIC-Biotech/ChemLib

From: Schultz, James  
 Sent: Thursday, May 15, 2003 7:52 AM  
 To: STIC-Biotech/ChemLib  
 Subject: Seq Search 09/780,929

RECEIVED

MAY 15 2003

Hello,  
 Could you please run a length limited nucleotide sequence search on SEQ ID NOS: 97 (15 nt long) and 98 (18 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 20 nucleotides long?  
 Thanks,  
 Doug Schultz

STIC-BIOTECH/CHEMLIB  
(STIC)

## STIC-Biotech/ChemLib

From: Schultz, James  
 Sent: Thursday, May 15, 2003 7:53 AM  
 To: STIC-Biotech/ChemLib  
 Subject: But wait there's more--Seq Search 09/780,929

RECEIVED

MAY 15 2003

STIC-BIOTECH/CHEMLIB  
(STIC)

The sequence search request below was just submitted--I forgot to include that I also need the interference databases searched. Thanks,  
 Doug Schultz

-----Original Message-----

From: Schultz, James  
 Sent: Thursday, May 15, 2003 7:52 AM  
 To: STIC-Biotech/ChemLib  
 Subject: Seq Search 09/780,929

Hello,  
 Could you please run a length limited nucleotide sequence search on SEQ ID NOS: 97 (15 nt long) and 98 (18 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 20 nucleotides long?  
 Thanks,  
 Doug Schultz

## TYPE OF SEARCH:

Searcher: \_\_\_\_\_  
 Phone: \_\_\_\_\_  
 Location: \_\_\_\_\_  
 Date Picked Up: 5/16  
 Date Completed: 5/25  
 Searcher Prep/Review: \_\_\_\_\_  
 Clerical: \_\_\_\_\_  
 Online time: \_\_\_\_\_

NA Sequences: \_\_\_\_\_  
 AA Sequences: \_\_\_\_\_  
 Structures: \_\_\_\_\_  
 Bibliographic: \_\_\_\_\_  
 Litigation: \_\_\_\_\_  
 Full text: \_\_\_\_\_  
 Patent Family: \_\_\_\_\_  
 Other: \_\_\_\_\_

## VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 Questel/Orbit: \_\_\_\_\_  
 DRLink: \_\_\_\_\_  
 Lexis/Nexis: \_\_\_\_\_  
 Sequence Sys.: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (specify): \_\_\_\_\_

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:53:27 ; Search time 871.364 Seconds

(Without alignments)  
500.987 Million cell updates/sec

Title: us-09-780-929-97

Perfect score: 15

Sequence: 1 aguaacgugaagau 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 332216

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_pa:\*

2: gb\_hlg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_hlg\_hum:\*

31: em\_hlg\_iny:\*

32: em\_hlg\_other:\*

33: em\_hlg\_mus:\*

34: em\_hlg\_pln:\*

35: em\_hlg\_rod:\*

36: em\_hlg\_mam:\*

37: em\_hlg\_vtl:\*

38: em\_sy:\*

39: em\_hlgo\_hum:\*

40: em\_hlgo\_mus:\*

41: em\_hlgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	15	100.0	15	6	AX214295	AX214295 Sequence
2	12	80.0	17	6	AX325565	AX325565 Sequence
3	12	80.0	17	6	AX325566	AX325566 Sequence
4	11	73.3	20	6	AX254729	AX254729 Sequence
5	11	73.3	20	6	AX255079	AX255079 Sequence
6	10.8	72.0	20	6	AX296064	AX296064 Sequence
7	10.8	72.0	20	6	AX304787	AX304787 Sequence
8	10.4	69.3	16	6	AX349237	AX349237 Sequence
9	10.4	69.3	17	6	AX272471	AX272471 Sequence
10	10.4	69.3	17	6	AX272472	AX272472 Sequence
11	10.4	69.3	17	6	AX272653	AX272653 Sequence
12	10.4	69.3	17	6	AX272654	AX272654 Sequence
13	10.4	69.3	17	6	AX272993	AX272993 Sequence
14	10.4	69.3	17	6	AX299883	AX299883 Sequence
15	10.4	69.3	17	6	AX325561	AX325561 Sequence
16	10.4	69.3	17	6	AX325562	AX325562 Sequence
17	10.2	68.0	15	6	AR033681	AR033681 Sequence
18	10.2	68.0	15	6	AR113503	AR113503 Sequence
19	10.2	68.0	15	6	I57910	I57910 Sequence 44
20	10.2	68.0	19	6	AR038557	AR038557 Sequence
21	10	66.7	16	6	A89154	A89154 Sequence 13
22	10	66.7	17	6	AX272473	AX272473 Sequence
23	10	66.7	18	6	AX110432	AX110432 Sequence
24	10	66.7	20	6	AX020035	AX020035 Sequence
25	10	66.7	20	6	AX295533	AX295533 Sequence
26	9.8	65.3	14	6	A15614	A15614 Oligonucleo
27	9.8	65.3	14	6	I04009	I04009 Sequence 5
28	9.8	65.3	15	6	AX008488	AX008488 Sequence
29	9.8	65.3	17	6	AR040477	AR040477 Sequence
30	9.8	65.3	17	6	AX227367	AX227367 Sequence
31	9.8	65.3	17	6	AX227387	AX227387 Sequence
32	9.8	65.3	18	6	A02405	A02405 Oligonucleo
33	9.8	65.3	18	6	AR106822	AR106822 Sequence
34	9.8	65.3	18	6	E32049	E32049 Antisense O
35	9.8	65.3	19	6	AX131036	AX131036 Sequence
36	9.8	65.3	19	6	AX131037	AX131037 Sequence
37	9.8	65.3	20	6	AR206662	AR206662 Sequence
38	9.8	65.3	20	6	AX148986	AX148986 Sequence
39	9.6	65.3	20	6	AX462586	AX462586 Sequence
40	9.6	64.0	17	6	AR162930	AR162930 Sequence
41	9.6	64.0	17	6	AR167259	AR167259 Sequence
42	9.6	64.0	17	6	AR206920	AR206920 Sequence
43	9.6	64.0	17	6	I33759	I33759 Sequence 5
44	9.6	64.0	17	6	I36972	I36972 Sequence 5
45	9.4	62.7	15	6	AR132924	AR132924 Sequence

## ALIGNMENTS

RESULT 1

AX214295

LOCUS AX214295

DEFINITION Sequence 108 from Patent WO0159102.

ACCESSION AX214295

VERSION AX214295.1 GI:15524372

KEYWORDS

SOURCE

ORGANISM

synthetic construct.

artificial sequences.

REFERENCE

1 (bases 1 to 15)

AUTHORS Breaker, R. and Emliss, G.

TITLE Nucleozymes with endonuclease activity

JOURNAL Patent: WO 0159102-A 108 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)

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FEATURES
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        /db_xref="taxon:32630"
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OY 1 AGAUAACGUGAGAU 15
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Db 1 AGATAACGTGAAGAT 15

RESULT 2
AX325565
LOCUS AX325565 17 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1703 from Patent WO0192512.
ACCESSION AX325565
VERSION AX325565.1 GI:18096322
KEYWORDS
SOURCE Beta vulgaris.
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.
REFERENCE
  1 Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
  Targeted chromosomal genomic alterations in plants using modified
  single stranded oligonucleotides
  Patent: WO 0192512-A 1703 06-DEC-2001;
  UNIVERSITY OF DELAWARE (US)
FEATURES
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        /db_xref="taxon:161934"
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  Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGUAACGUGAA 12
    |||:||||:||||
Db 4 AGATAACGTGAA 15

RESULT 3
AX325566/c
LOCUS AX325566 17 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1704 from Patent WO0192512.
ACCESSION AX325566
VERSION AX325566.1 GI:18096323
KEYWORDS
SOURCE Beta vulgaris.
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.
REFERENCE
  1 Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
  Targeted chromosomal genomic alterations in plants using modified
  single stranded oligonucleotides
  Patent: WO 0192512-A 1704 06-DEC-2001;
  UNIVERSITY OF DELAWARE (US)
FEATURES
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    Location/Qualifiers
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BASE COUNT      5 a      5 c      1 g      6 t
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Query Match
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OY 1 AGAUAACGUGAA 12
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Db 14 AGATAACGTGAA 3

RESULT 4
AX254729/c
LOCUS AX254729 20 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 18 from Patent WO0171027.
ACCESSION AX254729
VERSION AX254729.1 GI:16074396
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE
  1 (bases 1 to 20)
  Zohlnhofer, D., Baenerle, P., Klein, C. and Neumann, F.J.
  Mrna amplification
  Patent: WO 0171027-A 18 27-SEP-2001;
  Micromet AG (DE)
FEATURES
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BASE COUNT      4 a      6 c      5 g      5 t
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OY 5 AACGUGAGAU 15
    |||:||||:||||
Db 13 AACGTGAAGAT 3

RESULT 5
AX255079/c
LOCUS AX255079 20 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 18 from Patent WO0170953.
ACCESSION AX255079
VERSION AX255079.1 GI:16074565
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE
  1 (bases 1 to 20)
  Zohlnhofer, D., Baenerle, P., Klein, C. and Neumann, F.J.
  Identification of modulators of the interferon gamma signalling
  pathway and their use in restenosis treatment
  Patent: WO 0170953-A 18 27-SEP-2001;
  Micromet AG (DE)
FEATURES
  source
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      1. .20
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BASE COUNT      4 a      6 c      5 g      5 t
ORIGIN

Query Match
  Best Local Similarity 73.3%; Score 11; DB 6; Length 20;
  Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 AACGUGAGAU 15
    |||:||||:||||
Db 13 AACGTGAAGAT 3

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RESULT 6  
AX296064/C  
LOCUS AX296064 20 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 7826 from Patent WO0179548.  
ACCESSION AX296064  
VERSION AX296064.1 GI:17057753  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Barany,F., Zilvi,M., Gerry,N.P., Favis,R. and Kliman,R.  
TITLE Method of designing addressable array for detection of nucleic acid  
JOURNAL Sequence differences using ligase detection reaction  
PATENT: WO 0179548-A 7826 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
FEATURES  
source 1..20  
1. /organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Hypothetical Probe Sequence"  
BASE COUNT 4 a 7 c 4 g 5 t  
ORIGIN

Query Match 72.0%; Score 10.8; DB 6; Length 20;  
Best Local Similarity 64.3%; Pred. No. 2.7e+05;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAGAU 15  
1 :|||||1111:  
Db 15 GCTACGTCAGAGAT 2

RESULT 7  
AX304787/C  
LOCUS AX304787 20 bp DNA linear PAT 11-DEC-2001  
DEFINITION Sequence 22 from Patent EP1158045.  
ACCESSION AX304787  
VERSION AX304787.1 GI:17644468  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Schneider,Y.J. and Burtan,N.  
TITLE Culture conditions allowing to modulate the expression of cyp3a4 in  
JOURNAL Patent: EP 1158045-A 22 28-NOV-2001;  
UNIVERSITE CATHOLIQUE DE LOUVAIN (BE)  
FEATURES  
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/note="Oligonucleotide"  
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Best Local Similarity 64.3%; Pred. No. 2.7e+05;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAGAU 15  
1 :|||||1111:  
Db 20 GCTACGTCAGAGAT 7

RESULT 8  
AX349237/C  
LOCUS AX349237 16 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 21 from Patent WO0202810.  
ACCESSION AX349237

VERSION AX349237.1 GI:18615269  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Bickel,R., Ehrlich,R., Ellinger,T., Ernautraut,E., Kaiser,T.,  
Schulz,T. and Wagner,G.  
TITLE Method for qualitative and/or quantitative detecting of molecular  
JOURNAL interactions on probe arrays  
PATENT: WO 0202810-A 21 10-JAN-2002;  
Clondiaag Chip Technologies GmbH (DE)  
FEATURES  
source 1..16  
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Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 UACGUGAGAU 15  
1 :|||||1111:  
Db 13 TAAGCTGAGAGAT 2

RESULT 9  
AX272471/C  
LOCUS AX272471 17 bp mRNA linear PAT 29-OCT-2001  
DEFINITION Sequence 40 from Patent WO0162911.  
ACCESSION AX272471  
VERSION AX272471.1 GI:16545208  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlowitz,I., Mcswigen,J.A., Hamblin,P.A. and  
Ellis,J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 40 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)  
FEATURES  
source 1..17  
1. /organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 6 a 5 c 2 g 4 t  
ORIGIN

Query Match 69.3%; Score 10.4; DB 6; Length 17;  
Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 UACGUGAGAU 15  
1 :|||||1111:  
Db 16 TAAGCTGAGAGAT 5

RESULT 10  
AX272472/C  
LOCUS AX272472 17 bp mRNA linear PAT 29-OCT-2001  
DEFINITION Sequence 41 from Patent WO0162911.  
ACCESSION AX272472  
VERSION AX272472.1 GI:16545209  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.



```

REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mowiggen,J.A., Hamblin,P.A. and
          Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 41 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 UAACGUGAAGAU 15
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Db 15 TAACGTGAAGCT 4

RESULT 11
LOCUS AX272653 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 222 from Patent WO0162911.
ACCESSION AX272653
VERSION AX272653.1 GI:16545390
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mowiggen,J.A., Hamblin,P.A. and
          Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 222 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
SOURCE Location/Qualifiers
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BASE COUNT 6 a 5 c 2 g 4 t
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Query Match 69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 UAACGUGAAGAU 15
:||||:||||:
Db 17 TAACGTGAAGCT 6

RESULT 12
LOCUS AX272654 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 223 from Patent WO0162911.
ACCESSION AX272654
VERSION AX272654.1 GI:16545391
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mowiggen,J.A., Hamblin,P.A. and
          Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 223 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
SOURCE Location/Qualifiers

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Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 UAACGUGAAGAU 15
:||||:||||:
Db 14 TAACGTGAAGCT 3

RESULT 13
LOCUS AX272993 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 562 from Patent WO0162911.
ACCESSION AX272993
VERSION AX272993.1 GI:16545730
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mowiggen,J.A., Hamblin,P.A. and
          Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 562 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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ORIGIN
Query Match 69.3%; Score 10.4; DB 6; Length 17;
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OY 4 UAACGUGAAGAU 15
:||||:||||:
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RESULT 14
LOCUS AX299883 17 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 24 from Patent WO0183790.
ACCESSION AX299883
VERSION AX299883.1 GI:17129374
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Conner,T.W., Dubois,P., Malven,M. and Masucci,J.D.
TITLE Plant regulatory sequences for selective control of gene expression
JOURNAL Patent: WO 0183790-A 24 08-NOV-2001;
FEATURES Monsanto Technology LLC (US)
SOURCE Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Fully synthesized Primer"
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Best Local Similarity 83.3%; Pred. No. 4.6e+05;

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Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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 |||||  
 Db 16 GACACGTGAG 5

## RESULT 15

AX325561

LOCUS AX325561

17 bp DNA

linear

PAT 07-JAN-2002

DEFINITION Sequence 1699 from Patent WO0192512.

ACCESSION AX325561

VERSION AX325561.1 GI:18096318

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris.

Beta vulgaris.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Caryophyllaceae; Chenopodiaceae; Beta.

1

REFERENCE

AUTHORS

TITLE

JOURNAL

Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.

Targeted chromosomal genomic alterations in plants using modified

single stranded oligonucleotides

Patent: WO 0192512-A 1699 06-DEC-2001;

UNIVERSITY OF DELAWARE (US)

Location/Qualifiers

1. 17

/organism="Beta vulgaris"

/db\_xref="taxon:161934"

BASE COUNT 6 a 0 c 5 g 6 t

ORIGIN

Query Match 69.3%; Score 10.4; DB 6; Length 17;

Best Local Similarity 75.0%; Pred. No. 4.6e+05;

Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAA 12

|||||

Db 4 AGATAATGTGAA 15

Search completed: May 22, 2003, 19:36:39

Job time : 876.364 secs

GenCore version 5.1.4-P5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:52:30 ; Search time 146.364 Seconds

(without alignments)  
230.795 Million cell updates/sec

Title: US-09-780-929-97

Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 1367302

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N.Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
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- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
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- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
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- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*
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- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	15	22	AA512347	DNA encoding deoxy
2	12	80.0	17	20	AA16478	Human TIE-2 subtr
3	12	80.0	17	24	ABK26343	Increased starch p
4	12	80.0	17	24	ABK26344	Increased starch p
5	11.4	76.0	13	23	ABF31424	Oligonucleotide SE
6	11.4	76.0	13	23	ABF31425	Oligonucleotide SE
7	11.4	76.0	13	23	ABF76054	Oligonucleotide SE
8	11.4	76.0	13	23	ABF76055	Oligonucleotide SE
9	11.4	76.0	20	20	AA203321	PCR primer used to

C	10	11	73.3	12	23	AB125946	Oligonucleotide pr
C	11	11	73.3	12	23	AB178740	Oligonucleotide pr
C	12	11	73.3	13	23	ABF60400	Oligonucleotide SE
C	13	11	73.3	13	23	ABF60401	Oligonucleotide SE
C	14	11	73.3	20	22	AB166878	Nucleotide sequenc
C	15	11	73.3	20	22	AAD19670	Desmin PCR primer
C	16	10.8	72.0	15	21	AA703673	Synthetic oligonuc
C	17	10.8	72.0	18	19	AAV03676	Human Jagged DNA 5
C	18	10.8	72.0	20	18	AA793936	Primer for exon 24
C	19	10.8	72.0	20	24	ABK2365	Human MDR3 RT-PCR
C	20	10.8	72.0	20	24	AB196106	Capture oligonucle
C	21	10.4	69.3	12	23	AB102382	Oligonucleotide pr
C	22	10.4	69.3	12	23	AB132691	Oligonucleotide pr
C	23	10.4	69.3	12	23	AB134918	Oligonucleotide pr
C	24	10.4	69.3	12	23	AB145308	Oligonucleotide pr
C	25	10.4	69.3	13	23	ABC89900	Oligonucleotide SE
C	26	10.4	69.3	13	23	ABC89901	Oligonucleotide SE
C	27	10.4	69.3	13	23	ABF01726	Oligonucleotide SE
C	28	10.4	69.3	13	23	ABF01727	Oligonucleotide SE
C	29	10.4	69.3	16	24	AAK8514	Nucleic acid quant
C	30	10.4	69.3	17	21	AAF06199	Hammerhead ribozym
C	31	10.4	69.3	17	24	ABK26339	Increased starch p
C	32	10.4	69.3	17	24	ABK26340	Increased starch p
C	33	10.4	69.3	17	24	AA596503	Primer #21 used in
C	34	10.4	69.3	19	24	ABL56526	Nucleotide sequenc
C	35	10.4	69.3	20	21	AA60125	Hepatitis B virus
C	36	10.2	68.0	15	21	AA262836	Substrate for HH r
C	37	10.2	68.0	19	18	AA76452	Hepatitis GB virus
C	38	10.2	68.0	19	20	AAK81934	Probe used to dete
C	39	10.2	68.0	19	21	AA269809	Human biallelic ma
C	40	10.2	68.0	20	20	AAK32303	Oligo 3 used in co
C	41	10.2	68.0	20	21	AAD00965	Primer PAD4.31 to
C	42	10	66.7	10	22	AAE39878	Yeast NORF gene SA
C	43	10	66.7	12	23	ABH97436	Oligonucleotide pr
C	44	10	66.7	13	23	ABC19636	Oligonucleotide SE
C	45	10	66.7	13	23	ABC19637	Oligonucleotide SE

#### ALIGNMENTS

RESULT 1	AA512347	standard: DNA; 15 BP.
ID	AA512347	
AC	AA512347	
XX		
DT	21-NOV-2001	(first entry)
XX		
DE	DNA encoding deoxyribozyme #7.	
XX		
KW	Deoxyribozyme; cytosstatic; endonuclease; RNA cleavage; DNA cleavage;	
KW	gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.	
OS	Synthetic.	
XX		
PN	WO200159102-A2.	
XX		
PD	16-AUG-2001.	
XX		
PF	08-FEB-2001; 2001WO-US04223.	
XX		
PR	08-FEB-2000; 2000US-0181360.	
XX		
PR	31-MAR-2000; 2000US-0193646.	
XX		
PA	(RIBO-) RIBOZYME PHARM INC.	
XX	(UYVA) UNIV YALE.	
XX		
PI	Breaker R, Beigelman L, Emilsson G;	
XX		
DR	WPI; 2001-536526/59.	
XX		
PT	New nucleic acids with endonuclease activity, such as ribozymes and	

PT nucleozymes, for modulating gene expression in a plant, mammalian,  
bacterial or fungal cell -  
XX  
PS Claim 49; Page 77; 96pp; English.  
XX  
CC The invention relates to nucleic acid molecules with endonuclease  
CC activity, which are particularly useful for cleavage of RNA or DNA.  
CC The nucleic acids are used in a pharmaceutical composition and are used  
CC to modulate expression of a gene in a plant, mammalian, bacterial or  
CC fungal cell. They are used to cleave a separate nucleic acid, preferably  
CC RNA. The nucleic acids are used to inhibit gene expression and/or cell  
CC proliferation, and can be used to treat a disease or condition. More  
CC than one nucleic acid can be independently targeted to the same or  
CC different sites in a cell. The nucleic acids may be used to study DNA.  
CC The modifications to the nucleic acids optimises their catalytic activity  
CC and can maintain or enhance their activity. They exhibit a high degree  
CC of specificity for RNA. The present sequence represents the coding  
CC sequence of deoxyribozyme #7 used in the method of the invention.  
XX  
SQ Sequence 15 BP; 7 A; 1 C; 4 G; 3 U; 0 other;  
SO  
Query Match 100.0%; Score 15; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AGAUAACGUGAAGAU 15  
DB 1 AGAUAACGUGAAGAU 15  
|||||  
RESULT 2  
ID AAA18478 standard; RNA; 17 BP.  
XX  
AC AAA18478;  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Human TIE-2 substrate sequence SEQ ID NO:1704.  
XX  
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
KM integrin alpha 6 subunit; integrin subunit beta 3; halpin ribozyme;  
KM hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;  
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
KM age related macular degeneration; inflammation; neovascular glaucoma;  
KM myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;  
KM tuberosus scleriosis; pot-wine stain; Sturge Weber syndrome;  
KM Kippel-Trennauy-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
XX  
XX Homo sapiens.  
XX  
XX MO9950403-A2.  
XX  
XX 07-OCT-1999.  
XX  
XX 24-MAR-1999; 99MO-US06507.  
XX  
XX 27-MAR-1998; 98US-0079678.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwigen JA;  
XX WPI; 1999-591315/50.  
XX  
XX Novel ribozymes for modulating the synthesis, expression and/or  
XX stability of an mRNA encoding an angiogenic factors -  
XX  
XX Claim 56; Page 97; 305pp; English.  
XX  
XX The present invention describes enzymatic nucleic acid molecules with  
XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl

CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
CC AAA21596 to AAA21688 represent their corresponding target sequences;  
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
CC AAA23422 represent their corresponding target sequences. The ribozymes of  
CC the invention are used for modulating the synthesis, expression and/or  
CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
CC especially used to treat cancer, diabetic retinopathy, age related  
CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
CC angiodiroma of tuberosus scleriosis, pot-wine stains, Sturge Weber  
CC syndrome, Kippel-Trennauy-Weber syndrome, Osler-Weber-Rendu syndrome,  
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
CC integrin subunit alpha-6, or integrin subunit beta-3.  
XX  
SQ Sequence 17 BP; 7 A; 2 C; 6 G; 2 U; 0 other;  
SO  
Query Match 80.0%; Score 12; DB 20; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AGAUAACGUGAA 12  
DB 5 AGAUAACGUGAA 16  
|||||  
RESULT 3  
ID ABR26343  
XX  
XX ABR26343 standard; DNA; 17 BP.  
XX  
AC ABR26343;  
XX  
XX 09-APR-2002 (first entry)  
XX  
DE Increased starch production genome altering oligonucleotide #195.  
XX  
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
KM o-methyl modification; LNA modification; phosphorothioate linkage;  
KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
KM antibiotic stress tolerance; improved nutritional value; hygromycin; primer;  
KM amino acid over production; herbicide resistance; glyphosate resistance;  
KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
KM porphyric herbicide resistance; triazine resistance; disease resistance;  
KM modified oil production; modified starch production; wax starch;  
KM altered floral morphology; male-sterile plant; albino mutant;  
KM modified fatty acid content; reduced palmitate production; albino plant;  
KM increased stearate production; reduced linoleic acid production;  
KM photosynthetic process.  
XX  
XX Beta vulgaris.  
XX  
XX Synthetic.  
XX  
XX WO200192512-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 01-JUN-2001; 2001WO-US17672.  
XX  
XX 01-JUN-2000; 2000US-208538P.  
XX  
XX 30-OCT-2000; 2000US-244889P.  
XX  
XX 27-MAR-2001; 2001US-0818875.  
XX  
XX (UYDE ) UNIV DELAWARE.

PI Kmiec EB, Gamper HB, Rice MC, Kim J;  
 XX WPI; 2002-106307/14.  
 XX  
 PT New oligonucleotides with modified nuclease-resistant termini, useful  
 PT for creating plants with desired phenotypes, e.g. stress tolerance,  
 PT improved nutritional value, herbicide or disease resistance, or  
 PT modified oil production  
 XX  
 PS Claim 7, Page 145; 220pp; English.

CC The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention.  
 XX

SO Sequence 17 BP; 6 A; 1 C; 5 G; 5 T; 0 other;

Query Match 80.0%; Score 12; DB 24; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 3.2e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAUAACGUGAA 12  
 ||:||||:|  
 Db 4 AGATAACGTGAA 15

#### RESULT 4

ABK26344/C  
 ID ABK26344 standard; DNA; 17 BP.

AC ABK26344;

DT 09-APR-2002 (first entry)

DE Increased starch production genome altering oligonucleotide #196.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KM o-methyl modification; LNA modification; phosphorothioate linkage;  
 KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KM abiotic stress tolerance; improved nutritional value; hygromycin-B;  
 KM amino acid over production; herbicide resistance; glyphosate resistance;  
 KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KM porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KM modified oil production; modified starch production; waxy starch;  
 KM altered floral morphology; male-sterile plant; albino mutant;  
 KM modified fatty acid content; reduced palmitate production; albino plant;  
 KM increased stearate production; reduced linolenic acid production;  
 KM photosynthetic process.

OS Beta vulgaris.  
 OS Synthetic.

WO2001192512-A2.

PD 06-DEC-2001.  
 XX  
 XX 01-JUN-2001; 2001WO-US17672.  
 XX  
 PR 01-JUN-2000; 2000US-208538P.  
 PR 30-OCT-2000; 2000US-244989P.  
 PR 27-MAR-2001; 2001US-081887S.  
 XX  
 RA (UYDE ) UNIV DELAWARE.  
 XX  
 XX Kmiec EB, Gamper HB, Rice MC, Kim J;  
 XX WPI; 2002-106307/14.  
 XX  
 PT New oligonucleotides with modified nuclease-resistant termini, useful  
 PT for creating plants with desired phenotypes, e.g. stress tolerance,  
 PT improved nutritional value, herbicide or disease resistance, or  
 PT modified oil production  
 XX

PS Claim 7; Page 145; 220pp; English.

CC The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention.  
 XX

SO Sequence 17 BP; 5 A; 5 C; 1 G; 6 T; 0 other;

Query Match 80.0%; Score 12; DB 24; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 3.2e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAUAACGUGAA 12  
 ||:||||:|  
 Db 14 AGATAACGTGAA 3

#### RESULT 5

ABF31424  
 ID ABF31424 standard; DNA; 13 BP.

AC ABF31424;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 131421 for detecting SNP TSC0032802.

XX SNF: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.

WO200177384-A2.

PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB00713.  
XX  
XX 07-APR-2000; 2000DE-1019173.  
XX  
XX (EPIC-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
PS  
PS Claim 1; SEQ ID 131421; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 13 BP; 5 A; 1 C; 5 G; 2 T; 0 other;  
XX  
XX Query Match 76.0%; Score 11.4; DB 23; Length 13;  
XX Best Local Similarity 76.9%; Pred. No. 6.8e+03;  
XX Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 AGAUAACGUGAG 13  
DB 1 AGATAACGTGAG 13  
XX  
XX RESULT 6  
XX ABE31425/C  
XX ID ABE31425 standard; DNA; 13 BP.  
XX  
XX ABE31425;  
AC  
XX 21-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide SEQ ID NO 131422 for detecting SNP TSC0032802.  
DE  
XX  
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB00713.  
XX  
XX 07-APR-2000; 2000DE-1019173.  
XX  
XX (EPIC-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT

PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
PS  
PS Claim 1; SEQ ID 131422; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 13 BP; 2 A; 5 C; 1 G; 5 T; 0 other;  
XX  
XX Query Match 76.0%; Score 11.4; DB 23; Length 13;  
XX Best Local Similarity 76.9%; Pred. No. 6.8e+03;  
XX Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 AGAUAACGUGAG 13  
DB 13 AGATAACGTGAG 1  
XX  
XX RESULT 7  
XX ABE76054  
XX ID ABE76054 standard; DNA; 13 BP.  
XX  
XX ABE76054;  
AC  
XX 22-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide SEQ ID NO 176051 for detecting SNP TSC0043704.  
DE  
XX  
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB00713.  
XX  
XX 07-APR-2000; 2000DE-1019173.  
XX  
XX (EPIC-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
PS  
PS Claim 1; SEQ ID 176051; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and



XX Oligonucleotide primer SEQ ID NO 325919 for detecting SNP TSC0032801.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-1B00713.  
 XX 07-APR-2000; 2000DE-1019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single nucleotide polymorphisms and cytosine  
 XX methylation status  
 XX Claim 1; SEQ ID 325919; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 XX and cytosine methylation status in chemically pretreated genomic DNA. The  
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 XX range of diseases including immune system, gastrointestinal, respiratory,  
 XX central nervous system, cardiovascular and metabolic disorders. The  
 XX oligomers are also used for detecting cell type differentiation.  
 XX ABC00010-ABC99989, ABP00010-ABP99989, ABH00010-ABH99989 and  
 XX ABIO0010-ABIO82073 represent the oligomers described in the invention.  
 XX NOTE: The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 12 BP: 2 A; 4 C; 1 G; 5 T; 0 other;  
 XX  
 XX Query Match 73.3%; Score 11; DB 23; Length 12;  
 XX Best local Similarity 81.8%; Pred. No. 1.1e+04;  
 XX Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0  
 XX  
 XX 1 AGAUAACGUA 11  
 XX |||:||||:|  
 XX 12 AGATAACGTGA 2  
 XX  
 XX RESULT 11  
 XX ABI78740  
 XX ID ABI78740 standard; DNA: 12 BP.  
 XX ABI78740;  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide primer SEQ ID NO 378713 for detecting SNP TSC0006271.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-1B00713.

XX	07-APR-2000; 2000DE-1019173.
PR	(EPIC-) EPIGENOMICS AG.
XX	
PA	Olek A, Piepenbrock C, Berlin K;
PI	WPI: 2001-657177/75.
DR	
XX	
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single nucleotide polymorphisms and cytosine
PT	methylation status
XX	
PS	Claim 1; SEQ ID 378713; 29pp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligomers are also used for detecting cell type differentiation.
CC	ABCO0010-ABCG9989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC	ABI00010-ABI82073 represent the oligomers described in the invention.
CC	NOTE: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 12 BP; 5 A; 1 C; 3 G; 3 T; 0 other;
Query Match	73.3%; Score 11; DB 23; Length 12;
Best Local Similarity	81.8%; Pred. NO. 1.1e+04;
Matches	9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY	3 AUAACGUGAG 13
	I::IIII::IIII
DB	1 ATRACGTGAG 11
RESULT 12	
ABF60400	
ID	ABF60400 standard; DNA; 13 BP.
XX	
AC	ABF60400;
XX	
DT	22-FEB-2002 (first entry)
XX	
DE	Oligonucleotide SEQ ID NO 160397 for detecting SNP TSC0040381.
XX	
SNP	SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	
PN	WO200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-1B00713.
XX	
PR	07-APR-2000; 2000DE-1019173.
XX	
PA	(EPIC-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
DR	WPI: 2001-657177/75.
XX	
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single nucleotide polymorphisms and cytosine
PT	methylation status
XX	



PS Claim 1: SEQ ID 160397; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 13 BP; 6 A; 1 C; 3 G; 3 T; 0 other;  
  
Query Match 73.3%; Score 11; DB 23; Length 13;  
Best Local Similarity 81.8%; Pred. No. 1.1e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
OY 3 AUAACGUGAG 13  
1:|||||1111  
2 AUAACGTGAG 12  
DB  
  
RESULT 13  
ABF60401/c  
ID ABF60401 standard; DNA; 13 BP.  
XX  
AC ABF60401;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 160398 for detecting SNP TSC0040381.  
XX  
DE SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB00713.  
XX  
PR 07-APR-2000; 2000DE-1019173.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
WI: 2001-657177/75.  
DR  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status  
XX  
PS Claim 1: SEQ ID 160398; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABI00010-ABI82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 13 BP; 3 A; 3 C; 1 G; 6 T; 0 other;  
XX  
Query Match 73.3%; Score 11; DB 23; Length 13;  
Best Local Similarity 81.8%; Pred. No. 1.1e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
OY 3 AUAACGUGAG 13  
1:|||||1111  
12 AUAACGTGAG 2  
DB  
  
RESULT 14  
AAI66878/c  
ID AAI66878 standard; DNA; 20 BP.  
XX  
AC AAI66878;  
XX  
DT 07-JAN-2002 (first entry)  
XX  
DE Nucleotide sequence of primer seq id No. 18.  
XX  
KW Nucleic acid amplification; hybridization assay; interaction assay;  
KW expression cloning; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200171027-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-EP03311.  
XX  
PR 24-MAR-2000; 2000EP-0106450.  
XX  
PA (MICR-) MICROMET AG.  
XX  
PI Zohlhoefer D, Klein C;  
XX  
WI: 2001-611514/70.  
DR  
XX  
PT A method for the amplification of mRNA from a sample, e.g. for the  
PT preparation of in vitro surrogates for pathologically modified cells or  
PT tissues  
XX  
PS Examples; Page 168; 170pp; English.  
XX  
CC The invention provides a novel method for the amplification of mRNA from  
CC a sample. The method comprises (1) generating cDNA from polyadenylated  
CC RNA employing at least 1 primer hybridizing to the polyadenylated RNA and  
CC comprising a 5' poly(C) or a 5' poly(G) flank; (2) (either: (a)  
CC (optionally): (1) (if present) removing non-hybridized, surplus primer(s)  
CC and/or surplus dNTPs; (1b) 3' tailing of the generated cDNA with a poly  
CC (G) tail when in step (1) primer(s) comprising a 5' poly(C) flank was/  
CC were employed or a poly(C) tail when in step (1) primer(s) comprising a  
CC 5' poly(G) flank was/were employed; or (b) (optionally) 3' tailing of the  
CC generated cDNA with a poly(G) tail when in step (1) primer(s) comprising  
CC a 5' poly(C) flank was/were employed or a poly(C) tail when in step (1)  
CC primer(s) comprising a 5' poly(G) flank was/were employed using an RNA-  
CC ligase, irrespective of the presence or absence of surplus primer(s) and  
CC /or surplus dNTPs; and (3) amplifying the tailed cDNA with a primer  
CC hybridizing to the tails generated in step (2a) or (2b). The amplified  
CC cDNA obtained may be used for in vitro and/or in vivo expression and  
CC preparation of mRNA transcripts (which may then be used in hybridization  
CC assays (comprising hybridization to oligonucleotide arrays, cDNA arrays  
CC and/or PNA arrays) and/or interaction assays (comprising interactions  
CC with carbohydrates, lectins, ribozymes, proteins, peptides, antibodies  
CC and/or aptamers)) and for sequence specific PCR, cDNA cloning,  
CC subtractive hybridization cloning and/or expression cloning. Sequences  
CC AAI66876-890 represent primers used in the method of the invention.  
XX  
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Search completed: May 22, 2003, 19:04:24  
 Job time : 148.364 secs

Query Match 73.3%; Score 11; DB 22; Length 20;  
 Best Local Similarity 81.8%; Pred. No. 1.2e+04;  
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 AACGUGAAGAU 15  
 |||||  
 DB 13 AACGTGAAGAT 3

## RESULT 15

AAD19670/c  
 ID AAD19670 standard; DNA; 20 BP.

AC AAD19670;

DT 18-DEC-2001 (first entry)

DE Desmin PCR primer #2 related to the invention.

KW Inhibitor; interferon-gamma; IFN-gamma signalling pathway; therapy;

KW restenosis; coronary artery; carotid artery; femoralis artery;

KW aorta-coronary vein bypass; arterial bypass; venous bypass;

KW balloon angioplasty; stent implantation; vasotropic; PCR primer; ss.

OS Unidentified.

PN MO200170953-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-EP03312.

PR 24-MAR-2000; 2000EP-0106468.

PA (MICR-) MICROMET AG.

PI Zohlhoefer D, Baueerle P, Klein C, Neumann F;

DR WPI; 2001-616404/71.

PT Use of an inhibitor of the interferon gamma signalling pathway for  
 preparation of a pharmaceutical composition useful in the treatment or  
 prevention of restenosis -

PS Example 5; Page 55; 151pp; English.

CC The present invention relates to the use of an inhibitor of the  
 CC interferon-gamma (IFN-gamma) signalling pathway for the preparation of  
 CC a pharmaceutical composition for the treatment or prevention of  
 CC restenosis. The inhibitor is useful for the preparation of a  
 CC pharmaceutical composition useful in treating or preventing restenosis  
 CC which include restenosis of coronary arteries, carotid arteries,  
 CC femoralis arteries, aorta-coronary vein bypass, arterial bypass,  
 CC and/or venous bypass; and restenotic modification, where prevention  
 CC of restenotic modification is done before, during and/or after balloon  
 CC angioplasty and/or stent implantation and the restenosis or restenotic  
 CC modification is in-stent restenosis; and for treating and preventing  
 CC restenosis in a subject preferably human. The present sequence is a  
 CC desmin PCR primer which is used in aberrant gene expression in human  
 CC restenotic tissue used in the exemplification of the invention.

SO Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 73.3%; Score 11; DB 22; Length 20;

Best Local Similarity 81.8%; Pred. No. 1.2e+04;  
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 AACGUGAAGAU 15  
 |||||  
 DB 13 AACGTGAAGAT 3

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:32:43 ; Search time 1093.18 Seconds

(without alignments)  
222.225 Million cell updates/sec

Title: US-09-780-929-97

Perfect score: 15

Sequence: 1 agaaacgugaagaa 15

Scoring table:

IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 5800

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rdg:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	10.2	68.0	19	17	AZ759898
2	8.8	58.7	19	17	AZ465132
3	8.6	57.3	19	17	AZ603744
4	8.6	57.3	20	9	AU254575
5	8.4	56.0	20	17	AZ501985
6	8.2	54.7	19	14	C21102

7	8.2	54.7	19	17	AZ436629	AZ436629	1M0224019
8	8.2	54.7	19	17	AZ658282	AZ658282	1M0535C02
9	8.2	54.7	19	17	AZ983624	AZ983624	2M0264A22
10	8.2	54.7	20	17	AZ583235	AZ583235	1M0578J08
11	7.8	52.0	19	17	AZ331326	AZ331326	1M0059B15
12	7.8	52.0	19	17	AZ345449	AZ345449	1M0080J08
13	7.8	52.0	19	17	AZ245511	AZ245511	1M0080J01
14	7.8	52.0	19	17	AZ345536	AZ345536	1M0080006
15	7.8	52.0	19	17	AZ345572	AZ345572	1M0080017
16	7.8	52.0	19	17	AZ346709	AZ346709	1M0082M06
17	7.8	52.0	19	17	AZ346710	AZ346710	1M0082N01
18	7.8	52.0	19	17	AZ368837	AZ368837	1M0119A11
19	7.8	52.0	19	17	AZ414372	AZ414372	1M0186G18
20	7.8	52.0	19	17	AZ447223	AZ447223	1M0244H13
21	7.8	52.0	19	17	AZ447247	AZ447247	1M0244G19
22	7.8	52.0	19	17	AZ510096	AZ510096	1M0354B22
23	7.8	52.0	19	17	AZ510106	AZ510106	1M0354E19
24	7.8	52.0	19	17	AZ638980	AZ638980	1M0499L08
25	7.8	52.0	19	17	AZ954985	AZ954985	2M0220H21
26	7.6	50.7	20	17	AZ403838	AZ403838	1M0171K09
27	7.6	50.7	20	17	AZ462631	AZ462631	1M0269F12
28	7.6	50.7	20	17	AZ476391	AZ476391	1M0295F10
29	7.4	49.3	19	9	AU061154	AU061154	1M0295F10
30	7.4	49.3	19	13	BM397047	BM397047	5009-0-28
31	7.4	49.3	19	13	AZ496805	AZ496805	1M0333G22
32	7.2	48.0	19	9	A1439934	A1439934	t163c04.x
33	7.2	48.0	19	17	AZ319924	AZ319924	1M0039C15
34	7.2	48.0	19	17	AZ375600	AZ375600	1M0129K06
35	7.2	48.0	20	9	AU011147	AU011147	1M011147
36	7.2	48.0	20	17	AZ641695	AZ641695	1M0504E22
37	7.2	48.0	20	17	AZ807038	AZ807038	2M0069C06
38	7.2	48.0	20	17	AZ835078	AZ835078	2M0129E07
39	7.2	46.7	18	14	C21336	C21336	HDMS00037
40	7.2	46.7	18	14	C21365	C21365	HDMS000515
41	7.2	46.7	18	14	D11637	D11637	HDMS000318
42	7.2	46.7	19	9	AU061154	AU061154	1M061154
43	7.2	46.7	19	17	AZ588918	AZ588918	1M0397J05
44	7.2	46.7	19	17	AZ772819	AZ772819	1M0584F02
45	7.2	46.7	19	17	AZ783477	AZ783477	2M0025D18

## ALIGNMENTS

RESULT 1  
LOCUS  
DEFINITION  
1M0553A08F Mouse 10kb plasmid UGCLM library Mus musculus genomic  
clone UGCLM0553A08 F, DNA sequence.

ACCESSION  
AZ759898  
VERSION  
AZ759898.1 GI:12867157

KEYWORDS  
GSS.

SOURCE  
house mouse.

ORGANISM  
Mus musculus

REFERENCE  
AUTHORS

TITLE  
JOURNAL

COMMENT

19 bp DNA linear GSS 16-FEB-2001  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00



Plate: 0423 row: E column: 15  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1..19

BASE COUNT  
 ORIGIN  
 9 a 2 c 5 g 3 t  
 Query Match 57.3%; Score 8.6; DB 17; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 5.7e+05;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 1 AGAUAACGUGAAGAU 15  
 4 AAATCAGCGGAAAT 18

RESULT 4  
 AU254575/c 20 bp mRNA linear EST 25-Apr-2002  
 LOCUS AU254575 3'-directed mouse cDNA library Mus musculus cDNA clone  
 DEFINITION BDD0002532 3', mRNA sequence.  
 ACCESSION AU254575  
 VERSION AU254575.1 GI:20316485  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Kato, K. and Matoba, R.  
 Generation of expressed sequence tags from mouse brain  
 Unpublished (2002)  
 Contact: Kikuya Kato  
 Graduate School of Biological Sciences  
 Nara Institute of Science and Technology  
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
 Tel: 81-743-72-5581  
 Fax: 81-743-72-5589  
 Email: kato@bs.ist-nara.ac.jp,  
 URL: http://love2.aist-nara.ac.jp/BDD/index.html.  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
 /clone="BDD0002532"

/clone\_lib="3'-directed mouse cDNA library"  
 /tissue\_type="brain"  
 /note="Vector: pGEM-T-easy"  
 BASE COUNT 5 a 3 c 3 g 3 t  
 ORIGIN  
 Query Match 57.3%; Score 8.6; DB 9; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 5.9e+05;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 1 AGAUAACGUGAAGAU 15  
 16 AAAAGCGTGAAGAT 2

RESULT 5  
 AU2501985 20 bp DNA linear GSS 05-OCT-2000  
 LOCUS AU2501985 1M0341K05F Mouse 10kb plasmid UGCLM library Mus musculus genomic  
 DEFINITION clone UGCLM0341K05 F, DNA sequence.  
 ACCESSION AU2501985  
 VERSION AU2501985.1 GI:10683301  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Ismail, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10Kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0341 row: K column: 05  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: Plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCLM0341K05"  
 /clone\_lib="Mouse 10kb plasmid UGCLM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g114732114[gb|AF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

FEATURES  
 SOURCE  
 1..20  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="BDD0002532"

adapored vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 56.0%; Score 8.4; DB 17; Length 20;

Best Local Similarity 70.0%; Pred. No. 7.6e+05;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

LOCUS C21102 19 bp mRNA linear EST 23-OCT-1996  
DEFINITION HUMGS0002625 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA  
sequence.

ACCESSION C21102  
VERSION C21102.1 GI:1622212

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 19)

AUTHORS Okubo, K.  
TITLE BodyMap: human gene expression database  
JOURNAL Unpublished (1995)  
COMMENT Contact: Okubo, K.  
Institute for Molecular and Cellular Biol  
Osaka University  
1-3, Yamadaoka, Suita, Osaka Pref. 565, Japan  
Tel: 06-877-5111(ex.3315)  
Email: kousakueimcb.osaka-u.ac.jp

Human Gene Signature, 3'-directed cDNA sequence. We are not  
submitting the same cDNA sequence redundantly to DDBJ since 1993.  
For the abundance information of clones with this sequence in this  
library and as well as in other 3'-directed libraries, 'see '  
http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones  
represented by this GS sequences is also found there.

FEATURES  
source Location/Qualifiers

1..19  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human adult (K.Okubo)"  
/dev\_stage="adult"  
/note="Organ: blood; Vector: 1-gt-11; Site: 1: Eco-RI;  
Monocytes were prepared from blood by ficoll-hypaque,  
percoll and T cell rosetting purification steps (purity:  
96 %). mRNA was prepared from activated monocytes from a  
patient with rheumatoid arthritis. mRNA was reverse  
transcribed with MLV. Using Eco-RI linkers cDNA was  
cloned into 1-gt-11 vector arms. The cDNA library was  
screened by differential hybridization using radioactively  
marked ss-cDNA from activated and non-activated  
monocytes."

BASE COUNT 4 a 5 c 1 g 8 t 1 others

ORIGIN

Query Match 54.7%; Score 8.2; DB 14; Length 19;

Best Local Similarity 53.8%; Pred. No. 9.5e+05;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AUAACGUGAAGAU 15

Db 14. ATAAATGAGGAT 2

RESULT 7  
AZ436629

LOCUS AZ436629 19 bp DNA linear GSS 03-OCT-2000  
DEFINITION IM0224019P Mouse 10kb plasmid U06C1M library Mus musculus genomic  
clone U06C1M0224019 F, DNA sequence.

ACCESSION AZ436629  
VERSION AZ436629.1 GI:10560642

KEYWORDS GSS

SOURCE house mouse.

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0224 row: 0 column: 19  
Seq primer: CGTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source Location/Qualifiers

1..19  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06C1M0224019"  
/clone\_lib="Mouse 10kb plasmid U06C1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (9147321149b1AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapored mouse DNA was annealed to  
adapored vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 5 a 1 c 8 g 5 t

ORIGIN

Query Match 54.7%; Score 8.2; DB 17; Length 19;

Best Local Similarity 69.2%; Pred. No. 9.5e+05;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUACGUGAAGA 14

Db 7 GAGAACTGATGA 19

RESULT 8  
AZ658282/c

LOCUS A2658282 19 bp DNA linear GSS 14-DEC-2000  
 DEFINITION 1M0535C02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0535C02 F, DNA sequence.  
 ACCESSION A2658282  
 VERSION A2658282.1 GI:11795428  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0535 row: C column: 02  
 Seq primer: CGGTGAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

# FEATURES

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 1..19  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0535C02"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g14732114[gb|AF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 8 a 4 c 2 g 5 t  
 ORIGIN

Query Match 54.7%; Score 8.2; DB 17; Length 19;  
 Best Local Similarity 53.8%; Pred. No. 9.5e+05;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Oy 3 AGAACGCGAGAU 15  
 1:1 1:1 1:1  
 Db 17 ATATCTGAAATAT 5

RESULT 9  
 A2983624/c

LOCUS A2983624 19 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0264A22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0264A22 R, DNA sequence.  
 ACCESSION A2983624  
 VERSION A2983624.1 GI:13854851  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0264 row: A column: 22  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

# FEATURES

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 1..19  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0264A22"  
 /clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g14732114[gb|AF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 5 a 6 c 1 g 7 t  
 ORIGIN

Query Match 54.7%; Score 8.2; DB 17; Length 19;  
 Best Local Similarity 69.2%; Pred. No. 9.5e+05;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 AGAUAACGGAAG 13  
 1:1 1:1 1:1  
 Db 13 AGATTAATGACGAG 1

RESULT 10  
 A2583235

LOCUS AZ583235 20 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0378J08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0378J08 F, DNA sequence.  
 ACCESSION AZ583235  
 VERSION AZ583235.1 GI:11702915  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0378 row: J column: 08  
 Seq primer: CGTTGTAACGACGCGCGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers  
 1..20  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0378J08"  
 /clone.lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (g114732114|gblAF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 8 a 5 c 3 g 4 t  
 ORIGIN

Query Match 54.7%; Score 8.2; DB 17; Length 20;  
 Best Local Similarity 61.5%; Pred. No. 9.8e+05;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 AGAUAACGUGAAG 13  
 | | | | | | | | | |  
 DB 8 AAATACCTGAG 20

RESULT 11  
 AZ331326/c

LOCUS AZ313326 19 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0059B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0059B15 F, DNA sequence.  
 ACCESSION AZ313326  
 VERSION AZ313326.1 GI:10393927  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0059 row: B column: 15  
 Seq primer: CGTTGTAACGACGCGCGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1..19  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0059B15"  
 /clone.lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (g114732114|gblAF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 4 a 9 c 0 g 6 t  
 ORIGIN

Query Match 52.0%; Score 7.8; DB 17; Length 19;  
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAA 12  
 | | | | | | | | | |  
 DB 13 GGTAAAGTGA 3

RESULT 12  
 AZ345449/c



LOCUS	AZ345449	19 bp	DNA	linear	GSS 29-SEP-2000
DEFINITION	IM0080108F Mouse 10kb plasmid cDNA library Mus musculus genomic clone UUCG1M0080108 F, DNA sequence.				
ACCESSION					
VERSION	AZ345449				
KEYWORDS					
SOURCE	AZ345449.1	GI:10424686			
ORGANISM	GSS. house mouse. Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rogace,R., Stokes,R., Tinger,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112 USA  Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0080 row: I column: 08 Seq primer: CGTCTAATAAGCAGCCGCACGT Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1..19				
FEATURES					
SOURCE	1..19				

BASE COUNT  
ORIGIN

4 a g c 0 g 6 t

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/oranism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UCM0080108"
/clone_1lb="Mouse 10kb plasmid uuc01m library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match	52.08;	Score 7.8;	DB 17;	Length 19;
Best Local Similarity	63.68;	Pred. No. 1.6e+06;		
Matches	7;	Conservative	2;	Mismatches 0;
				Gaps 0;

QY	2	GAUAACGUGAA	12
		:     :	
Db	13	GGTAAGGTGAA	3

RESULT 13  
AZ345511/C

LOCUS	AZ245511	19 bp	DNA	linear	GSF 29-SEP-2000
DEFINITION	1M0080J01F Mouse 10kb plasmid U0GC1M library Mus musculus genomic				
ACCESSION	clone U0GC1M0080J01 F, DNA sequence.				
VERSION	AZ245511				
KEYWORDS	GSF.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,				
	Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly				
	,M., Rose,M., Rogase,R., Stokes,R., Tingey,A., von Niederhausern,A.				
	and Wright,D., Weiss,R..				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb				
	plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
	University of Utah				
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT				
	84112, USA				
	Tel: 801 585 5606				
	Fax: 801 585 7177				
	Email: ddunn@genetics.utah.edu				
	Insert Length: 10000 Std Error: 0.00				
	Plate: 0080 row: J column: 01				
	Seq primer: CGTGTAAACGACGCGCCAGT				
	Class: plasmid end				
FEATURES	High quality sequence stop: 19.				
SOURCE	1..19				
	Location/Qualifiers				

BASE COUNT  
ORIGIN

4 a 9 c 0 g 6 t

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/organism="Mus musculus"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="U9C1M0080J01"  
/clone_id="Mouse 10kb plasmid U9C1M library"  
/sex="Male"  
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42ny; Purified genomic DNA from M.  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g114731141gb1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."
```

Query Match	52.0%;	Score 7.8;	DB 17;	Length 19;
Best Local Similarity	63.6%;	Pred. NO. 1.6e+06;		
Matches	7;	Conservative	2;	Mismatches 2;
			Indels	0;
			Gaps	0;

QY	2	GAUAACGUGAA	12
		:      :	
Db	13	GCTAAGGTGAA	3

RESULT 14  
AZ345536/c

LOCUS AZ345536 19 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0080006F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0080006 F, DNA sequence.  
 ACCESSION AZ345536  
 VERSION AZ345536.1 GI:10424773  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0080 row: 0 column: 06  
 Seq primer: CGTTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 FEATURES  
 source  
 1. 19  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0080006"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g11473211419b1AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## BASE COUNT

4 a 9 c 0 g 6 t

## ORIGIN

Query Match 52.0%; Score 7.8; DB 17; Length 19;  
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUAACGUGAA 12  
 1 : 11 1 : 11 1  
 Db 13 GGTAAGCTGAA 3

RESULT 15  
 AZ345572/c

LOCUS AZ345572 19 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0080017F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0080017 F, DNA sequence.  
 ACCESSION AZ345572  
 VERSION AZ345572.1 GI:10424809  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0080 row: 0 column: 17  
 Seq primer: CGTTGTAAACGACGCCACGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 FEATURES  
 source  
 1. 19  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0080017"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g11473211419b1AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## BASE COUNT

4 a 9 c 0 g 6 t

Query Match 52.0%; Score 7.8; DB 17; Length 19;  
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUAACGUGAA 12  
 1 : 11 1 : 11 1  
 Db 13 GGTAAGCTGAA 3

Search completed: May 22, 2003, 20:17:01  
 Job time : 1100.18 secs





CURRENT FILING DATE: 2001-02-08  
NUMBER OF SEQ ID NOS: 154  
SEQ ID NO: 22  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-780-175-22

Query Match 72.0%; Score 10.8; DB 4; Length 20;  
Best Local Similarity 64.3%; Pred. No. 1.8e+03;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAUACGUGAAGAU 15  
1 : |||:|||||:  
Db 20 GCGACGTGAGAGAT 7

## RESULT 3

US-08-182-968A-447/C  
Sequence 447, Application US/08182968A  
Patent No. 5610054

## GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 447:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-447

Query Match 68.0%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 3.8e+03;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15  
|||:|||||:  
Db 15 AGATAACGACAGAGT 1

RESULT 4  
US-08-774-306A-447/C  
Sequence 447, Application US/08774306A  
Patent No. 5869253

## GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,306A  
FILING DATE: December 26, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 447:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-306A-447

Query Match 68.0%; Score 10.2; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 3.8e+03;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15  
|||:|||||:  
Db 15 AGATAACGACAGAGT 1

## RESULT 5

US-09-064-156A-447/C  
Sequence 447, Application US/09064156A  
Patent No. 6132966

## GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 498  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/064.156A  
FILING DATE: April 21, 1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/774.306  
FILING DATE: December 26, 1996  
APPLICATION NUMBER: 08/182.968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882.888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 234/083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 447:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-064-156A-447

Query Match 68.0%; Score 10.2; DB 3; Length 15;  
Best Local Similarity 66.7%; Pred. No. 3.8e+03;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15  
|||:|||||  
Db 15 AGATAACGACAAGCT 1

RESULT 6  
US-08-580-038-29  
Sequence 29, Application US/08580038  
Patent No. 5807670  
GENERAL INFORMATION:  
APPLICANT: Muethoff, A. S.  
APPLICANT: Simons, J. N.  
APPLICANT: Birkenmeyer, L.  
APPLICANT: Leary, T. P.  
APPLICANT: Leary, J. C.  
APPLICANT: Desai, S. M.  
APPLICANT: Mushahwar, I. K.  
APPLICANT: Chalmers, M.  
APPLICANT: Dawson, G. J.  
TITLE OF INVENTION: Detection of Hepatitis GB Virus  
TITLE OF INVENTION: Genotypes  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Rd  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/580.038  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Foremski, Priscilla E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5793.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-0378  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-580-038-29

Query Match 68.0%; Score 10.2; DB 1; Length 19;  
Best Local Similarity 66.7%; Pred. No. 3.9e+03;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15  
|||:|||||  
Db 4 AGAGAGGTTAAGAT 18

RESULT 7  
US-09-780-175-50/c  
Sequence 50, Application US/09780175  
Patent No. 6440738  
GENERAL INFORMATION:  
APPLICANT: Robert McKay  
APPLICANT: Susan M. Freier  
APPLICANT: Jacqueline Wyatt  
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION  
FILE REFERENCE: RTS-0164  
CURRENT APPLICATION NUMBER: US/09/780.175  
CURRENT FILING DATE: 2001-02-08  
NUMBER OF SEQ ID NOS: 154  
SEQ ID NO 50  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-780-175-50

Query Match 66.7%; Score 10; DB 4; Length 20;  
Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAAGAU 15  
|||:|||||  
Db 19 ACGTGAAGAT 10

RESULT 8  
US-08-758-306-1325/c  
Sequence 1325, Application US/08758306  
Patent No. 5807743  
GENERAL INFORMATION:  
APPLICANT: Slinchcomb, Dan T.  
APPLICANT: McSwiggen, James A.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH  
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
NUMBER OF SEQUENCES: 1379  
CORRESPONDENCE ADDRESS:

QY	2	GAUACGUGAGA	14
		:	
Db	18	GAAAGGTGAAGA	6

RESULT 12  
 US-08-180-2098-5  
 ; Sequence 5, Application US/08180209B  
 ; Patent No. 5593877  
 ; GENERAL INFORMATION:  
 ; APPLICANT: King, Te-Piao  
 ; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
 ; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
 ; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED  
 ; TITLE OF INVENTION: THEREON  
 ; NUMBER OF SEQUENCES: 62  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Klauder & Jackson  
 ; STREET: 411 Hackensack Avenue  
 ;

CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/180,209B  
FILING DATE: 11-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/031,400  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-074 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-180-209B-5

Query Match  
Best Local Similarity 64.0%; Score 9.6; DB 1; Length 17;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUACGUGAGAU 15  
DB 1 GAYACNGTNARAT 14

RESULT 13  
US-08-385-745-5  
Sequence 5, Application US/08385745  
Patent No. 5612209  
GENERAL INFORMATION:  
APPLICANT: King, Te Piao  
TITLE OF INVENTION: Cloning and Recombinant Production of  
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/385,745  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,400  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 3288-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-385-745-5

Query Match  
Best Local Similarity 64.0%; Score 9.6; DB 1; Length 17;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUACGUGAGAU 15  
DB 1 GAYACNGTNARAT 14

RESULT 14  
US-08-485-388-5  
Sequence 5, Application US/08485388  
Patent No. 6270763  
GENERAL INFORMATION:  
APPLICANT: King, Te Piao  
TITLE OF INVENTION: Cloning and Recombinant Production of  
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,388  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/385,745  
FILING DATE: 08-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/031,400  
FILING DATE: 11-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-074 FWCA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA



US-08-485-388-5

## Query Match

64.0%; Score 9.6; DB 4; Length 17;

Best Local Similarity 50.0%; Pred. No. 8.3e+03;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUACGUGAGAU 15

DB 1 GAYACGCTNARAT 14

## RESULT 15

US-08-474-853-5

Sequence 5, Application US/08474853

Patent No. 6287559

## GENERAL INFORMATION:

APPLICANT: King, Te-Piao

TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND

TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON

NUMBER OF SEQUENCES: 62

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber &amp; Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,853

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/180,209

FILING DATE: 11-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/031,400

FILING DATE: 11-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-074 CIPB

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-474-853-5

## Query Match

64.0%; Score 9.6; DB 4; Length 17;

Best Local Similarity 50.0%; Pred. No. 8.3e+03;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUACGUGAGAU 15

DB 1 GAYACGCTNARAT 14

Search completed: May 22, 2003, 20:18:23  
Job time : 35.2727 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:36:48 ; Search time 70.9091 Seconds

(Without alignments)  
279.329 Million cell updates/sec

Title: US-09-780-929-97  
Perfect score: 15  
Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 191488

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
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2: /cgn2\_6/ptodata/1/pubpna/PC7\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/PC7US\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PC7US\_PUBCOMB.seq:\*  
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8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
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12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	US-09-780-929-97	Sequence 97, Appl
2	10.8	72.0	17	US-09-730-2898-606	Sequence 606, App
3	10.8	72.0	17	US-09-730-2898-607	Sequence 607, App
4	10.8	72.0	18	US-10-213-329-4	Sequence 4, Appl
5	10.4	69.3	19	US-09-969-373-2697	Sequence 2697, Ap
6	10.2	68.0	15	US-09-504-231A-469	Sequence 469, App
7	10.2	68.0	15	US-09-274-553D-469	Sequence 469, App
8	10.2	68.0	19	US-10-000-773A-6	Sequence 6, Appl
9	9.8	65.3	17	US-09-776-474-739	Sequence 739, App
10	9.8	65.3	17	US-09-776-474-959	Sequence 959, App
11	9.8	65.3	20	US-09-918-187-64	Sequence 64, Appl
12	9.8	65.3	20	US-09-800-631-141	Sequence 141, App
13	9.4	62.7	17	US-09-730-2898-596	Sequence 596, App
14	9.4	62.7	18	US-09-878-582-29	Sequence 29, Appl
15	9.4	62.7	18	US-09-969-373-4497	Sequence 4497, Ap
16	9.4	62.7	19	US-09-969-373-1862	Sequence 1862, Ap
17	9.4	62.7	20	US-09-917-963-42	Sequence 42, Appl
18	9.4	62.7	20	US-09-953-611-56	Sequence 56, Appl
19	9.4	62.7	20	US-09-752-983-112	Sequence 112, App

C	20	9.4	62.7	20	US-09-908-500A-15	Sequence 15, Appl
	21	9.2	61.3	15	US-09-825-805-150	Sequence 150, Appl
	22	9.2	61.3	15	US-09-365-029-87	Sequence 87, Appl
	23	9.2	61.3	15	US-09-365-029-88	Sequence 88, Appl
C	24	9.2	61.3	16	US-09-365-029-5	Sequence 11, Appl
	25	9.2	61.3	16	US-09-365-029-11	Sequence 25, Appl
	26	9.2	61.3	17	US-08-908-884-25	Sequence 525, App
	27	9.2	61.3	17	US-09-825-805-525	Sequence 103, App
	28	9.2	61.3	17	US-09-730-2898-103	Sequence 833, App
	29	9.2	61.3	17	US-09-730-2898-835	Sequence 1081, Ap
	30	9.2	61.3	17	US-09-730-2898-1081	Sequence 935, App
	31	9.2	61.3	17	US-09-848-754A-935	Sequence 936, App
	32	9.2	61.3	17	US-09-848-754A-936	Sequence 2185, Ap
	33	9.2	61.3	17	US-09-848-754A-2185	Sequence 74, Appl
	34	9.2	61.3	17	US-09-776-474-74	Sequence 426, App
	35	9.2	61.3	17	US-09-776-474-426	Sequence 427, App
	36	9.2	61.3	17	US-09-776-474-427	Sequence 25, Appl
	37	9.2	61.3	17	US-09-908-323-25	Sequence 89, Appl
	38	9.2	61.3	18	US-09-925-598-89	Sequence 89, Appl
	39	9.2	61.3	18	US-09-805-761-22	Sequence 22, Appl
	40	9.2	61.3	18	US-09-889-293A-89	Sequence 89, Appl
	41	9.2	61.3	18	US-09-889-735-89	Sequence 89, Appl
	42	9.2	61.3	18	US-09-900-444-89	Sequence 89, Appl
	43	9.2	61.3	18	US-09-989-730-89	Sequence 89, Appl
	44	9.2	61.3	18	US-09-990-436-89	Sequence 89, Appl
	45	9.2	61.3	18	US-09-991-181-89	Sequence 89, Appl

## ALIGNMENTS

RESULT 1  
US-09-780-929-97  
Sequence 97, Application US/09780929  
Patent No. US20020151693A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc  
APPLICANT: Breaker, Ronald  
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity  
FILE REFERENCE: MHHB00-884-H (500/001)  
CURRENT APPLICATION NUMBER: US/09/780, 929  
PRIOR FILING DATE: 2001-02-08  
PRIOR APPLICATION NUMBER: US 60/181,360  
NUMBER OF SEQ ID NOS: 126  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 97  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-929-97  
Query Match 100.0%; Score 15; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 AGAUAACGUGAAGAU 15  
Db 1 AGAUAACGUGAAGAU 15  
RESULT 2  
US-09-730-2898-606/c  
Publication No. US20030050259A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwiggen, Jim  
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease

FILE REFERENCE: MBH00-864-A (400/006)  
CURRENT APPLICATION NUMBER: US/09/730,289B  
CURRENT FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: US 60/169,100  
PRIOR FILING DATE: 1999-12-06  
NUMBER OF SEQ ID NOS: 3897  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 606  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-730-289B-606

Query Match 72.0%; Score 10.8; DB 9; Length 17;  
Best Local Similarity 71.4%; Pred. No. 1.3e+04;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGA 14  
DB 17 AGATAACATGAGAGA 4

RESULT 3  
US-09-730-289B-607/C  
Sequence 607, Application US/09730289B  
Publication No. US20030050259A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwiggen, Jim  
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
FILE REFERENCE: MBH00-864-A (400/006)  
CURRENT APPLICATION NUMBER: US/09/730,289B  
CURRENT FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: US 60/169,100  
PRIOR FILING DATE: 1999-12-06  
NUMBER OF SEQ ID NOS: 3897  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 607  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-730-289B-607

Query Match 72.0%; Score 10.8; DB 9; Length 17;  
Best Local Similarity 71.4%; Pred. No. 1.3e+04;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGA 14  
DB 15 AGATAATGTGAGAGA 2

RESULT 4  
US-10-213-329-4  
Sequence 4, Application US/10213329  
Publication No. US20030083465A1  
GENERAL INFORMATION:  
APPLICANT: Zimrin, Ann B.  
APPLICANT: MacIsig, Thomas  
APPLICANT: Wong, Michael K.K.  
APPLICANT: Pepper, Michael S.  
APPLICANT: Montesano, Roberto  
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS  
FILE REFERENCE: BASED ON JAGED/NOTCH PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE: 0036-101  
CURRENT APPLICATION NUMBER: US/10/213,329  
CURRENT FILING DATE: 2002-08-06  
PRIOR APPLICATION NUMBER: US/09/199,865  
PRIOR FILING DATE: 1998-11-25  
PRIOR APPLICATION NUMBER: 60/018,841  
PRIOR FILING DATE: 1996-05-31  
PRIOR APPLICATION NUMBER: PCT/US97/09407

PRIOR FILING DATE: 1997-05-30  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: cDNA  
US-10-213-329-4

Query Match 72.0%; Score 10.8; DB 9; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1.3e+04;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAUAACGUGAAGAU 15  
DB 1 GAGACCGTGAAGAT 14

RESULT 5  
US-09-969-373-2697/C  
Sequence 2697, Application US/09969373  
Patent No. US20020133852A1  
GENERAL INFORMATION:  
APPLICANT: Efferitz, Roger J.  
APPLICANT: Haughe, Brian M.  
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
FILE REFERENCE: 38-10(52679)A  
CURRENT APPLICATION NUMBER: US/09/969,373  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US 09/754,853  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 09/760,427  
PRIOR FILING DATE: 2001-01-13  
PRIOR APPLICATION NUMBER: US 09/855,768  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 4593  
SEQ ID NO 2697  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-969-373-2697

Query Match 69.3%; Score 10.4; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 2.1e+04;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAA 12  
DB 17 AGACAACGTGAA 6

RESULT 6  
US-09-504-231A-469/C  
Sequence 469, Application US/09504231A  
Patent No. US20020013458A1  
GENERAL INFORMATION:  
APPLICANT: Blatt, Lawrence  
APPLICANT: McSwiggen, James  
APPLICANT: Roberts, Beth  
APPLICANT: Pavco, Pamela  
APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL  
FILE REFERENCE: HEPATITIS C VIRUS INFECTION  
FILE REFERENCE: rpl 247/282  
CURRENT APPLICATION NUMBER: US/09/504,231A  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 09/274,553  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24

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;; PRIOR APPLICATION NUMBER: 60/100,842
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/083,217
;; PRIOR FILING DATE: 1998-04-27
;; NUMBER OF SEQ ID NOS: 3242
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 469
;; LENGTH: 15
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-469

Query Match
Best Local Similarity 68.0%; Score 10.2; DB 10; Length 15;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15
DB 15 AGATAACGACAGGT 1

RESULT 7
US-09-274-553D-469/c
;; Sequence 469, Application US/09274553D
;; Patent No. US2002082225A1
;; GENERAL INFORMATION:
;; APPLICANT: Blatt, Lawrence
;; APPLICANT: McSwigen, James
;; APPLICANT: Roberts, Beth
;; APPLICANT: Pavco, Pamela
;; APPLICANT: Macejak, Dennis
;; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
;; FILE REFERENCE: rpi 247/282
;; CURRENT APPLICATION NUMBER: US/09/274,553D
;; CURRENT FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 09/257,608
;; PRIOR FILING DATE: 1999-02-24
;; PRIOR APPLICATION NUMBER: 60/100,842
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/083,217
;; PRIOR FILING DATE: 1998-04-27
;; NUMBER OF SEQ ID NOS: 3148
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 469
;; LENGTH: 15
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-469

Query Match
Best Local Similarity 68.0%; Score 10.2; DB 10; Length 15;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15
DB 15 AGATAACGACAGGT 1

RESULT 8
US-10-000-773A-6
;; Sequence 6, Application US/10000773A
;; Publication No. US20030069195A1
;; GENERAL INFORMATION:
;; APPLICANT: Farrar, Gwenyth Jane
;; APPLICANT: Humphries, Peter
;; APPLICANT: Kenna, Paul
;; APPLICANT: Millington-Ward, Sophia
;; TITLE OF INVENTION: Suppression of Polymorphic Alleles
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;; FILE REFERENCE: MUR-001CP
;; CURRENT APPLICATION NUMBER: US/10/000,773A
;; CURRENT FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: US 09/142,125
;; PRIOR FILING DATE: 1999-04-12
;; PRIOR APPLICATION NUMBER: PCT/GB97/00574
;; PRIOR FILING DATE: 1997-03-03
;; PRIOR APPLICATION NUMBER: GB 9604449.0
;; PRIOR FILING DATE: 1996-03-01
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 6
;; LENGTH: 19
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: 5' human collagen 1A2 primer
US-10-000-773A-6

Query Match
Best Local Similarity 68.0%; Score 10.2; DB 9; Length 19;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15
DB 2 AGAGATGCTGAAGAT 16

RESULT 9
US-09-776-474-739
;; Sequence 739, Application US/09776474
;; Publication No. US20030087847A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: Jarvis, Thale
;; APPLICANT: Booher, Robert
;; APPLICANT: Holman, Patricia
;; APPLICANT: Fattaey, All
;; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (
;; FILE REFERENCE: MBH00-955-A (400/008)
;; CURRENT APPLICATION NUMBER: US/09/776,474
;; CURRENT FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: US 60/179,983
;; PRIOR FILING DATE: 2000-03-02
;; NUMBER OF SEQ ID NOS: 2992
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 739
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-739

Query Match
Best Local Similarity 65.3%; Score 9.8; DB 9; Length 17;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAG 13
DB 2 AGAAAUUGUGAAG 14

RESULT 10
US-09-776-474-959
;; Sequence 959, Application US/09776474
;; Publication No. US20030087847A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: Jarvis, Thale
;; APPLICANT: Booher, Robert
```

```

; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 959
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-959

Query Match
Best Local Similarity 65.3%; Score 9.8; DB 9; Length 17;
Best Local Similarity 84.6%; Pred. No. 4.4e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAG 13
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DB 4 AGAAAUUGUGAG 16

RESULT 11
US-09-918-187-64
; Sequence 64, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-64

Query Match
Best Local Similarity 65.3%; Score 9.8; DB 9; Length 20;
Best Local Similarity 61.5%; Pred. No. 4.5e+04;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AUAACGUGAGAU 15
    ||| ||| |||
DB 4 ATATCTGGAAGAT 16

RESULT 12
US-09-800-631-141/C
; Sequence 141, Application US/09800631
; Patent No. US20020082228A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXPR
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/09/800,631
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 141
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-800-631-141

Query Match
Best Local Similarity 65.3%; Score 9.8; DB 10; Length 20;
Best Local Similarity 69.2%; Pred. No. 4.5e+04;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAG 13
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DB 13 AGATAACATGTAG 1

RESULT 13
US-09-730-289B-596
; Sequence 596, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 596
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-596

Query Match
Best Local Similarity 62.7%; Score 9.4; DB 9; Length 17;
Best Local Similarity 90.9%; Pred. No. 7.3e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AUAACGUGAG 13
    ||| ||| |||
DB 4 AUAACAUGAG 14

RESULT 14
US-09-878-582-29/C
; Sequence 29, Application US/09878582
; Patent No. US20020058638A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Robert McKay
; APPLICANT: Lex M. Cowseart
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
; FILE REFERENCE: ISPH-0463
; CURRENT APPLICATION NUMBER: US/09/878,582
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/577,902
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/358,381
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US99/29594,
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-878-582-29
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Query Match 62.7%; Score 9.4; DB 10; Length 18;  
Best Local Similarity 72.7%; Pred. No. 7.3e+04;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 AACGUGAAGAU 15  
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Db 17 AAGGTGAAGAT 7

## RESULT 15

US-09-969-373-4497/C  
; Sequence 4497, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Effertz, Roger J.  
; APPLICANT: Haug, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 4497  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Glycine max  
; US-09-969-373-4497

Query Match 62.7%; Score 9.4; DB 10; Length 18;  
Best Local Similarity 72.7%; Pred. No. 7.3e+04;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 GAUACGUGAA 12  
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Db 13 GATAACGTGCA 3

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Job time : 72.9091 secs

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:59:38 ; Search time 1728.64 Seconds

(without alignments)  
218.170 Million cell updates/sec

Title: US-09-780-929-97

Perfect score: 15  
Sequence: 1 agaaacgugaagaau 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 24791104 segs, 12571243825 residues

Total number of hits satisfying chosen parameters: 1600790

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_

1:	/cgn2_
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42:	/cgn2_
43:	/cgn2_

44:	/cgn2_6/ptodata/1/pna/US6000.COMB.seq:*
45:	/cgn2_6/ptodata/1/pna/US6001.COMB.seq:*
46:	/cgn2_6/ptodata/1/pna/US6002.COMB.seq:*
47:	/cgn2_6/ptodata/1/pna/US6003.COMB.seq:*
48:	/cgn2_6/ptodata/1/pna/US6004.COMB.seq:*
49:	/cgn2_6/ptodata/1/pna/US6005.COMB.seq:*
50:	/cgn2_6/ptodata/1/pna/US6006.COMB.seq:*
51:	/cgn2_6/ptodata/1/pna/US6007.COMB.seq:*
52:	/cgn2_6/ptodata/1/pna/US6008.COMB.seq:*
53:	/cgn2_6/ptodata/1/pna/US6009.COMB.seq:*
54:	/cgn2_6/ptodata/1/pna/US6010.COMB.seq:*
55:	/cgn2_6/ptodata/1/pna/US6011.COMB.seq:*
56:	/cgn2_6/ptodata/1/pna/US6012.COMB.seq:*
57:	/cgn2_6/ptodata/1/pna/US6013.COMB.seq:*
58:	/cgn2_6/ptodata/1/pna/US6014.COMB.seq:*
59:	/cgn2_6/ptodata/1/pna/US6015.COMB.seq:*
60:	/cgn2_6/ptodata/1/pna/US6016.COMB.seq:*
61:	/cgn2_6/ptodata/1/pna/US6017.COMB.seq:*
62:	/cgn2_6/ptodata/1/pna/US6018.COMB.seq:*
63:	/cgn2_6/ptodata/1/pna/US6019.COMB.seq:*
64:	/cgn2_6/ptodata/1/pna/US6020.COMB.seq:*

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the results. The split freed up more machine time for processing searches.

Pending Nucleic Acid Pending database produce two sets of results, with the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rapn  
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

*The Pending database search results should not be left in the case because they contain data that is confidential.*

10	10.8	72.0	18	22	US-09-730-289B-607	Sequence 50, App1
11	10.8	72.0	18	22	US-09-579-536-4	Sequence 606, App
12	10.8	72.0	18	22	US-09-579-536-4	Sequence 607, App
13	10.8	72.0	18	22	US-09-688-078-12	Sequence 4, App1
14	10.8	72.0	18	22	US-10-213-329-4	Sequence 12, App1
15	10.8	72.0	18	22	US-10-213-329-4	Sequence 4, App1
16	10.8	72.0	18	22	US-60-216-745-5964	Sequence 5964, App
17	10.8	72.0	18	22	PCT-US02-03159-22	Sequence 22, App1
18	10.8	72.0	18	22	US-09-068-506-50	Sequence 50, App1
19	10.8	72.0	18	22	US-09-514-000-12603	Sequence 12603, A
20	10.8	72.0	18	22	US-09-514-000-15028	Sequence 15028, A
21	10.8	72.0	18	22	US-09-703-708-12172	Sequence 12172, A
22	10.8	72.0	18	22	US-60-164-320-12172	Sequence 12172, A
23	10.8	72.0	18	22	US-60-183-791-12172	Sequence 12172, A
24	10.8	72.0	18	22	PCT-US98-26935-217	Sequence 217, App
25	10.8	72.0	18	22	US-09-215-436-217	Sequence 217, App

Query Match 72.0%; Score 10.8; DB 65; Length 18;  
 Best Local Similarity 64.3%; Pred. No. 1e+05;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAUACGUGAAGAU 15  
 ||:||||:| | | | |  
 DB 2 GATACCTGGAAGAT 15

RESULT 13  
 PCT-US02-03159-22/c  
 ; Sequence 22, Application PC/TUS0203159  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Isis Pharmaceuticals, Inc.  
 ; APPLICANT: Robert McKay  
 ; APPLICANT: Susan M. Preler  
 ; APPLICANT: Jacqueline Waitt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION  
 ; FILE REFERENCE: RISP-0270  
 ; CURRENT APPLICATION NUMBER: PCT/US02/03159  
 ; CURRENT FILING DATE: 2002-01-31  
 ; NUMBER OF SEQ ID NOS: 154  
 ; SEQ ID NO 22  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 PCT-US02-03159-22

Query Match 72.0%; Score 10.8; DB 1; Length 20;  
 Best Local Similarity 64.3%; Pred. No. 1e+05;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAUACGUGAAGAU 15  
 ||:||||:| | | | |  
 DB 20 GCTGACGTGAAGAT 7

RESULT 14  
 US-09-068-506-50/c  
 ; Sequence 50, Application US/09068506A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YASUE, Hirofumi  
 ; APPLICANT: YOSHIMURA, Kunamoto  
 ; TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH CORONARY  
 ; FILE REFERENCE: 0032-245P  
 ; CURRENT APPLICATION NUMBER: US/09/068,506A  
 ; CURRENT FILING DATE: 1998-07-10  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 50  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Primers  
 US-09-068-506-50

Query Match 72.0%; Score 10.8; DB 14; Length 20;  
 Best Local Similarity 64.3%; Pred. No. 1e+05;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAUACGUGAAGAU 15  
 ||:||||:| | | | |  
 DB 14 GGTACCTGAAGAT 1

RESULT 15  
 US-09-514-000-12603/c  
 ; Sequence 12603, Application US/09514000

; GENERAL INFORMATION:  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof  
 ; FILE REFERENCE: 38-10(15490)B  
 ; CURRENT APPLICATION NUMBER: US/09/514,000  
 ; CURRENT FILING DATE: 2000-02-23  
 ; NUMBER OF SEQ ID NOS: 15034  
 ; SEQ ID NO 12603  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Agrobacterium tumefaciens  
 US-09-514-000-12603

Query Match 72.0%; Score 10.8; DB 19; Length 20;  
 Best Local Similarity 64.3%; Pred. No. 1e+05;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAUACGUGAAGAU 15  
 ||:||||:| | | | |  
 DB 20 GATGACCTGAAGAT 7

Search completed: May 22, 2003, 21:22:03  
 Job time : 1731.64 secs



GenCore version 5.1.4-p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:04:38 ; Search time 371.364 Seconds  
(without alignments)  
209.509 Million cell updates/sec

Title: US-09-780-929-97

Perfect score: 15  
Sequence: 1 agauacgugaagau 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6438716 seqs, 2593467500 residues

Total number of hits satisfying chosen parameters: 667140

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_MN\_New:\*  
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2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq2:\*  
7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq3:\*  
8: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*  
9: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq2:\*  
10: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*  
11: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq2:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	11.8	78.7	20	9	US-10-316-389-88
C 2	11.4	76.0	20	1	PCT-US02-38622-50
C 3	11	73.3	15	9	US-10-287-818-374
C 4	11	73.3	15	9	US-10-287-818-836
C 5	10.8	72.0	19	9	US-10-310-188-47798
C 6	10.8	72.0	20	9	US-10-302-027-46
C 7	10.8	72.0	20	9	US-10-302-027-106
C 8	10.4	69.3	16	8	US-10-311-109-21
C 9	10.4	69.3	17	6	US-09-846-903-24
C 10	10.4	69.3	17	6	US-10-310-188-80491
C 11	10.4	69.3	19	1	PCT-US03-03662-97
C 12	10.4	69.3	19	1	PCT-US03-03662-336
C 13	10.4	69.3	19	9	US-10-310-188-14089
C 14	10.4	69.3	20	1	PCT-US02-38806-82
C 15	10.4	69.3	20	8	US-10-317-277A-73
C 16	10.4	69.3	20	8	US-10-317-277A-148
C 17	10.2	68.0	15	6	US-09-274-553E-469
C 18	10.2	68.0	17	9	US-10-310-188-22900
C 19	10.2	68.0	19	1	PCT-US02-34679-118
C 20	10.2	68.0	19	9	US-10-287-174-118
C 21	10.2	68.0	19	9	US-10-293-338-4500
C 22	10.2	68.0	19	9	US-10-349-143-4165

C 23	10.2	68.0	20	9	US-10-298-994-110	Sequence 110, App
C 24	10.2	68.0	20	9	US-10-298-994-212	Sequence 212, App
C 25	10.2	68.0	20	9	US-10-310-188-35003	Sequence 35003, A
C 26	10.2	68.0	20	9	US-10-317-249-86	Sequence 86, Appl
C 27	10.2	68.0	20	9	US-10-317-249-161	Sequence 161, App
C 28	10	66.7	15	1	PCT-US02-28539-2145	Sequence 2145, App
C 29	10	66.7	15	1	PCT-US02-28539-2146	Sequence 2146, App
C 30	10	66.7	15	1	PCT-US02-28539-3267	Sequence 3267, App
C 31	10	66.7	15	8	US-10-287-787-13654	Sequence 13654, A
C 32	10	66.7	15	9	US-10-305-276-1129	Sequence 1129, App
C 33	10	66.7	15	9	US-10-316-954-4481	Sequence 4481, App
C 34	10	66.7	15	9	US-10-316-954-5747	Sequence 5747, App
C 35	10	66.7	15	9	US-10-305-276A-1129	Sequence 1129, App
C 36	10	66.7	15	9	US-10-364-516-2145	Sequence 2145, App
C 37	10	66.7	15	9	US-10-364-516-2146	Sequence 2146, App
C 38	10	66.7	15	9	US-10-364-516-3267	Sequence 3267, App
C 39	10	66.7	15	9	US-10-364-516-3268	Sequence 3268, App
C 40	10	66.7	15	9	US-10-364-516-3268	Sequence 3268, App
C 41	10	66.7	15	9	US-10-089-177-1165	Sequence 1165, App
C 42	10	66.7	19	8	US-10-385-163-94	Sequence 94, Appl
C 43	10	66.7	19	11	US-60-453-420-94	Sequence 94, Appl
C 44	9.8	65.3	15	9	US-10-305-273-723	Sequence 723, App
C 45	9.8	65.3	15	9	US-10-305-273-1246	Sequence 1246, App

## ALIGNMENTS

RESULT 1  
US-10-316-389-88/c  
Sequence 88, Application US/10316389  
GENERAL INFORMATION:  
APPLICANT: Kenneth W. Doble  
TITLE OF INVENTION: ANTISENSE MODULATION OF ABC2 EXPRESSION  
FILE REFERENCE: PRT-0382  
CURRENT APPLICATION NUMBER: US/10/316, 389  
CURRENT FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 143  
SEQ ID NO 88  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-316-389-88

Query Match 78.7% Score 11.8; DB 9; Length 20;  
Best Local Similarity 80.0% Pred. No. 1.1e+04;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

0Y 1 AGAUACGUGAAGAU 15  
DB 15 AGACACGGGAAGAT 1  
RESULT 2  
PCT-US02-38622-50/c  
Sequence 50, Application PC/TUS0238622  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Susan M. Freiler  
TITLE OF INVENTION: ISIS Pharmaceuticals, Inc.  
FILE REFERENCE: PRSP-0447  
CURRENT APPLICATION NUMBER: PCT/US02/38622  
CURRENT FILING DATE: 2002-12-04  
PRIOR APPLICATION NUMBER: 10/003, 919  
PRIOR FILING DATE: 2001-12-06  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 50  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
PCT-US02-38622-50

Query Match  
Best Local Similarity 76.0%; Score 11.4; DB 1; Length 20;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GAUACGUGAGA 14  
|||:|||||  
Db 20 GACACGTGAGA 8

RESULT 3  
US-10-287-818-374  
Sequence 374, Application US/10287818  
GENERAL INFORMATION:

APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Vibrio cholerae chromosome I, complete chromosome.  
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/287,818  
CURRENT FILING DATE: 2002-11-05

NUMBER OF SEQ ID NOS: 1318  
SOFTWARE: Proprietary  
SEQ ID NO 374  
LENGTH: 15  
TYPE: DNA

ORGANISM: Vibrio cholerae chromosome I, complete chromosome.  
FEATURE:

LOCATION: (810101)...(810115)  
OTHER INFORMATION: Chromosome - 1 strand - positive ConnectonbjectNumber = 534  
US-10-287-818-374

Query Match  
Best Local Similarity 73.3%; Score 11; DB 9; Length 15;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 AACGUGAGAU 15  
||||:|||||  
Db 1 AACGTGAGAT 11

RESULT 4  
US-10-287-818-836  
Sequence 836, Application US/10287818  
GENERAL INFORMATION:

APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Vibrio cholerae chromosome I, complete chromosome.  
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/287,818  
CURRENT FILING DATE: 2002-11-05

NUMBER OF SEQ ID NOS: 1318  
SOFTWARE: Proprietary  
SEQ ID NO 836  
LENGTH: 15  
TYPE: DNA

ORGANISM: Vibrio cholerae chromosome I, complete chromosome.  
FEATURE:

LOCATION: (1812221)...(1812235)  
OTHER INFORMATION: Chromosome - 1 strand - negative ConnectonbjectNumber = 1169  
US-10-287-818-836

Query Match  
Best Local Similarity 73.3%; Score 11; DB 9; Length 15;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 AACGUGAGAU 15  
||||:|||||  
Db 1 AACGTGAGAT 11

RESULT 5  
US-10-310-188-47798

Sequence 47798, Application US/10310188  
GENERAL INFORMATION:

APPLICANT: Rosettacomics  
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G  
FILE REFERENCE: 47487  
CURRENT APPLICATION NUMBER: US/10/310,188  
CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 47798  
LENGTH: 19  
TYPE: DNA

ORGANISM: Homo sapiens  
US-10-310-188-47798

Query Match  
Best Local Similarity 72.0%; Score 10.8; DB 9; Length 19;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAGAU 15  
|||:|||||  
Db 2 GAGACATGAGAT 15

RESULT 6  
US-10-302-027-46/c  
Sequence 46, Application US/10302027  
GENERAL INFORMATION:

APPLICANT: Nicholas M. Dean  
TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION  
FILE REFERENCE: PTS-0068  
CURRENT APPLICATION NUMBER: US/10/302,027  
CURRENT FILING DATE: 2002-11-21

NUMBER OF SEQ ID NOS: 135  
SEQ ID NO 46  
LENGTH: 20  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide  
US-10-302-027-46

Query Match  
Best Local Similarity 72.0%; Score 10.8; DB 9; Length 20;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAGAU 15  
|||:|||||  
Db 14 GGTACTTGAAGAT 1

RESULT 7  
US-10-302-027-106  
Sequence 106, Application US/10302027  
GENERAL INFORMATION:

APPLICANT: Nicholas M. Dean  
TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION  
FILE REFERENCE: PTS-0068  
CURRENT APPLICATION NUMBER: US/10/302,027  
CURRENT FILING DATE: 2002-11-21

NUMBER OF SEQ ID NOS: 135  
SEQ ID NO 106  
LENGTH: 20  
TYPE: DNA

ORGANISM: H. sapiens  
FEATURE:

Query Match  
Best Local Similarity 72.0%; Score 10.8; DB 9; Length 20;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

US-10-302-027-106

Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAUACGUGAAGU 15  
1 :|||:|||||  
Db 7 GGTAATTGAAGAT 20

RESULT 8  
US-10-331-109-21/c  
; Sequence 21, Application US/10331109  
; GENERAL INFORMATION:  
; APPLICANT: Bickel, et al.  
; TITLE OF INVENTION: Method for the qualitative and/or quantitative detection of molec  
; FILE REFERENCE: 12671/1  
; CURRENT APPLICATION NUMBER: US/10/331.109  
; CURRENT FILING DATE: 2002-12-27  
; PRIOR APPLICATION NUMBER: PCT/EP01/07575  
; PRIOR FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: DE 100 33 334.6  
; PRIOR FILING DATE: 2000-07-01  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of the artificial sequence:  
US-10-331-109-21

Query Match  
Best Local Similarity 66.7%; Pred. No. 6.2e+04;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 UAACGUGAAGU 15  
1 :|||:|||||  
Db 13 TAAGTGAAGAT 2

RESULT 9  
US-09-846-903-24/c  
; Sequence 24, Application US/09846903  
; GENERAL INFORMATION:  
; APPLICANT: Connor, Timothy W.  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Malven, Marianne  
; APPLICANT: Masucci, James D.  
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL  
; FILE REFERENCE: 38-21(15678)B promoters  
; CURRENT APPLICATION NUMBER: US/09/846.903  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: US 60/201,255  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: fully  
; OTHER INFORMATION: synthesized primer  
US-09-846-903-24

Query Match  
Best Local Similarity 83.3%; Pred. No. 6.2e+04;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAUACGUGAAG 13  
1 :|||:|||||

Db 16 GACACGTGAAG 5

RESULT 10  
US-10-310-188-80491/c  
; Sequence 80491, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310.188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: Patentln version 3.1  
; SEQ ID NO 80491  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-80491

Query Match  
Best Local Similarity 75.0%; Pred. No. 6.2e+04;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AUACGUGAAGA 14  
1 :|||:|||||  
Db 15 ATAACGTGAAA 4

RESULT 11  
PCT-US03-03662-97/c  
; Sequence 97, Application PC/TUS0303662  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwigen, James  
; APPLICANT: Beigelman, Leonid  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Express  
; FILE REFERENCE: 02-1005-A (400/083)  
; CURRENT APPLICATION NUMBER: PCT/US03/03662  
; CURRENT FILING DATE: 2003-02-06  
; PRIOR APPLICATION NUMBER: US 60/411,275  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: Patentln version 3.2  
; SEQ ID NO 97  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sens  
PCT-US03-03662-97

Query Match  
Best Local Similarity 75.0%; Pred. No. 6.2e+04;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAGA 14  
1:1111111111  
DB 12 ATACGCTGAGA 1

RESULT 12  
PCT-US03-03662-336

; Sequence 336, Application PC/TUS0303662  
; GENERAL INFORMATION:  
; APPLICANT: Mbozyme Pharmaceuticals, Inc.  
; APPLICANT: Mbozyme, James  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Thompson, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression  
; FILE REFERENCE: 02-1005-A (400/083)  
; CURRENT APPLICATION NUMBER: PCT/US03/03662  
; CURRENT FILING DATE: 2003-02-06  
; PRIOR APPLICATION NUMBER: US 60/411,275  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 336  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense region  
PCT-US03-03662-336

Query Match 69.3%; Score 10.4; DB 1; Length 19;  
Best Local Similarity 91.7%; Pred. No. 6.2e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAGA 14  
1111111111  
DB 8 AUAACGUGAGA 19

RESULT 13  
US-10-310-188-14089  
; Sequence 14089, Application US/10310188  
; GENERAL INFORMATION:  
; APPLICANT: RosettaGenomics  
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE  
; FILE REFERENCE: 47487  
; CURRENT APPLICATION NUMBER: US/10/310,188  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 86841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14089  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-310-188-14089

Query Match 69.3%; Score 10.4; DB 9; Length 19;  
Best Local Similarity 83.3%; Pred. No. 6.2e+04;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 2 GAUACGUGAG 13  
1111111111  
DB 8 GATACGGGAG 19

RESULT 14  
PCT-US02-38806-82

; Sequence 82, Application PC/TUS0238806  
; GENERAL INFORMATION:  
; APPLICANT: University of Rochester  
; APPLICANT: Therianos, Stavros  
; APPLICANT: Coleman, Paul  
; APPLICANT: Zhu, Min  
; TITLE OF INVENTION: MULTIPLEX REAL-TIME QUANTITATIVE PCR  
; FILE REFERENCE: 21108.0009P1  
; CURRENT APPLICATION NUMBER: PCT/US02/38806  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/397,475  
; PRIOR FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 60/336,095  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: /note =  
PCT-US02-38806-82

Query Match 69.3%; Score 10.4; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 6.2e+04;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAGA 14  
1111111111  
DB 8 ACAACGTGAGA 19

RESULT 15  
US-10-317-277A-73/C  
; Sequence 73, Application US/10317277A  
; GENERAL INFORMATION:  
; APPLICANT: Dobie, Kenneth W.  
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression  
; FILE REFERENCE: RTS-0473  
; CURRENT APPLICATION NUMBER: US/10/317,277A  
; CURRENT FILING DATE: 2002-12-10  
; NUMBER OF SEQ ID NOS: 168  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 73  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Antisense oligonucleotide  
US-10-317-277A-73

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Best Local Similarity 75.0%; Pred. No. 6.2e+04;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAGA 14  
1111111111  
DB 20 ATACGCTGAGA 9

Search completed: May 22, 2003, 21:35:56  
Job time : 374.364 secs



GenCore version 5.1.4-p5-4578  
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## OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:53:27 ; Search time 1045.64 Seconds

(Without alignments)  
500.987 Million cell updates/sec

Title: US-09-780-929-98

Sequence: 1 aauggcnaucgugcga 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 332216

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_ov:\*

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7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rod:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	6	AX214296	AX214296 Sequence
2	12.8	71.1	20	6	AX295903	AX295903 Sequence
3	12.2	67.8	20	6	AX293899	AX293899 Sequence
4	11.8	65.6	20	6	AX293092	AX293092 Sequence
5	11.8	65.3	20	6	E30812	E30812 Novel prote
6	11.4	63.3	17	6	AR057682	AR057682 Sequence
7	11.4	63.3	17	6	AR057773	AR057773 Sequence
8	11.4	63.3	17	6	AR115440	AR115440 Sequence
9	11.4	63.3	17	6	AR115531	AR115531 Sequence
10	11.2	62.2	17	6	AX010333	AX010333 Sequence
11	11.2	62.2	17	6	AX215191	AX215191 Sequence
12	11.2	62.2	17	6	I05557	I05557 Sequence 1
13	10.8	60.0	20	6	AX293459	AX293459 Sequence
14	10.6	58.9	18	6	AX189338	AX189338 Sequence
15	10.6	58.9	20	6	AR063454	AR063454 Sequence
16	10.6	58.9	20	6	AX293222	AX293222 Sequence
17	10.4	57.8	15	6	AR033731	AR033731 Sequence
18	10.4	57.8	15	6	AR113553	AR113553 Sequence
19	10.4	57.8	15	6	I57960	I57960 Sequence 49
20	10.4	57.8	20	6	AX293280	AX293280 Sequence
21	10.4	57.8	20	6	AX294297	AX294297 Sequence
22	10.2	56.7	15	6	AR120152	AR120152 Sequence
23	10.2	56.7	17	6	AR190327	AR190327 Sequence
24	10.2	56.7	17	6	AR190328	AR190328 Sequence
25	10.2	56.7	17	6	AR190329	AR190329 Sequence
26	10.2	56.7	17	6	AX216858	AX216858 Sequence
27	10.2	56.7	17	6	AX217220	AX217220 Sequence
28	10.2	56.7	18	6	AR081732	AR081732 Sequence
29	10.2	56.7	19	6	I09664	I09664 Sequence 2
30	10.2	56.7	20	6	A79710	A79710 Sequence 6
31	10.2	56.7	20	6	AX293581	AX293581 Sequence
32	10.2	56.7	20	6	AX295607	AX295607 Sequence
33	10.2	56.7	20	6	AX452366	AX452366 Sequence
34	10.2	56.7	20	6	E43264	E43264 Primer for
35	10.2	56.7	20	6	E43283	E43283 Primer for
36	10.2	56.7	12	6	A92476	A92476 Sequence 7
37	10	55.6	12	6	AR106027	AR106027 Sequence
38	10	55.6	18	6	AX467000	AX467000 Sequence
39	10	55.6	20	6	AX278397	AX278397 Sequence
40	10	55.6	20	6	AX278439	AX278439 Sequence
41	10	55.6	20	6	AX294871	AX294871 Sequence
42	10	55.6	20	6	AX319927	AX319927 Sequence
43	10	55.6	20	6	I31196	I31196 Sequence 10
44	9.8	54.4	16	6	AR105448	AR105448 Sequence
45	9.8	54.4	17	6	AR190326	AR190326 Sequence

## ALIGNMENTS

RESULT 1

AX214296

LOCUS AX214296 18 bp mRNA

DEFINITION Sequence 109 from Patent WO0159102.

ACCESSION AX214296

VERSION AX214296.1 GI:15524373

KEYWORDS

ORGANISM

SOURCE

synthetic construct.

artificial sequences.

REFERENCE

1 (bases 1 to 18)

AUTHORS Breaker,R. and Emilsson,G.

TITLE Nucleozymes with endonuclease activity

PATENT: WO 0159102-A 109 16-AUG-2001;

JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)



PH Key Location/Qualifiers  
FT source 1. .20  
/organism='unidentified'.  
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source 1. .20  
Location/Qualifiers  
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Best Local Similarity 60.0%; Pred. No. 9.2e+04;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCUAVCGGCG 17  
Db 20 TGCGCTCGGTGCG 6

RESULT 6  
AR057682 17 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 1886 from patent US 5837542.  
ACCESSION AR057682  
VERSION AR057682.1 GI:5983259  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
Grimm,S., Stinchcomb,D.T., McSwigen,J., Sullivan,S. and  
Draper,K.G.  
TITLE Interleukin adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1886 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"

BASE COUNT 1 a 5 c 7 g 4 t  
ORIGIN

Query Match 63.3%; Score 11.4; DB 6; Length 17;  
Best Local Similarity 69.2%; Pred. No. 1.5e+05;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUAVCGGCG 16  
Db 2 GGCTGTGCGTGC 14

RESULT 7  
AR057773 17 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 1977 from patent US 5837542.  
ACCESSION AR057773  
VERSION AR057773.1 GI:5983350  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
Grimm,S., Stinchcomb,D.T., McSwigen,J., Sullivan,S. and  
Draper,K.G.  
TITLE Interleukin adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1977 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"

BASE COUNT 1 a 5 c 7 g 4 t  
ORIGIN

Query Match 63.3%; Score 11.4; DB 6; Length 17;  
Best Local Similarity 69.2%; Pred. No. 1.5e+05;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUAVCGGCG 16  
Db 2 GGCTGTGCGTGC 14

RESULT 8  
AR115440 17 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 1886 from patent US 6132967.  
ACCESSION AR115440  
VERSION AR115440.1 GI:14095762  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
Grimm,S., Stinchcomb,D.T., McSwigen,J., Sullivan,S. and  
Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of  
JOURNAL Interleukin adhesion molecule-1 (ICAM-1)  
FEATURES Patent: US 6132967-A 1886 17-OCT-2000;  
source 1. .17  
Location/Qualifiers  
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BASE COUNT 1 a 5 c 7 g 4 t  
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Query Match 63.3%; Score 11.4; DB 6; Length 17;  
Best Local Similarity 69.2%; Pred. No. 1.5e+05;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUAVCGGCG 16  
Db 2 GGCTGTGCGTGC 14

RESULT 10  
AX010333 17 bp DNA linear PAT 06-SEP-2000  
LOCUS Sequence 4 from Patent WO9960007.  
ACCESSION AX010333



VERSION	AX010333.1	GI:9997186
KEYWORDS	Bacteriophage M13mp18.	
SOURCE	Bacteriophage M13mp18	
ORGANISM	Viruses.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Hamilton,A.L., Shchepinoy,M.S., Southern,E.M., Elder,J.K. and Housby,J.N.	
TITLE	Reagent and method Patent: WO 960007-A 4 25-NOV-1996;	
JOURNAL	HAMILTON ALAN LEWIS (GB); SCHCHEPINOV MIKHAIL SERGEVICH (GB); SOUTHERN EDWIN MELLOR (GB); IJIS INNOVATION (GB); ELDER JOHN KENNETH (GB); HOUSBY JOHN NICHOLAS (GB)	
FEATURES	Location/Qualifiers	
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	/note="M13mp18 ssDNA"	
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Best Local Similarity	68.8%; Pred. No. 2e+05;	
Matches	11; Conservative	2; Mismatches 3; Indels 0; Gaps 0;
OY	2 AUGGCCUAGCGUGCG 17	
Db	1 AAGGCGCATCGCTGC 16	
RESULT 11		
AX215191/c		
LOCUS	AX215191	17 bp mRNA linear PAT 07-SEP-2001
DEFINITION	Sequence 633 from Patent WO0159103.	
ACCESSION	AX215191	
VERSION	AX215191.1	GI:15525234
KEYWORDS		
SOURCE		
ORGANISM	Synthetic construct.	
REFERENCE	Synthetic construct	
AUTHORS	artificial sequences.	
TITLE	1 (bases 1 to 17)	
JOURNAL	Blatt,L., Mcswigen,J. and Chowrira,B.M.	
FEATURES	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression	
SOURCE	Patent: WO 0159103-A 633 16-AUG-2001;	
	RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; Mcswigen, James (US) ; Chowrira, Bharat M. (US)	
	Location/Qualifiers	
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	/organism="synthetic construct"	
	/db_xref="taxon:32630"	
	/note="Nucleic Acid"	
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Query Match	62.2%; Score 11.2; DB 6;	Length 17;
Best Local Similarity	56.2%; Pred. No. 2e+05;	
Matches	9; Conservative	4; Mismatches 3; Indels 0; Gaps 0;
OY	1 AAUGCCUAGCGUGC 16	
Db	11:1 1:1:1 1:11	
	16 AATGATCATCTGTGC 1	
RESULT 12		
LOCUS	I05557	17 bp DNA linear PAT 02-DEC-1996
DEFINITION	Sequence 1 from Patent EP 0285123.	
ACCESSION	I05557	
VERSION	I05557.1	GI:590718
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	

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REFERENCE      1 (bases 1 to 17)
AUTHORS       Lehtovaara,P., Knowles,J., Koivula,A., Bamford,J. and
              Reinikainen,T.
TITLE         A method for complete mutagenesis of nucleic acids
JOURNAL       Patent: EP 0285123-A2 1 05-OCT-1988;
FEATURES      Location/Qualifiers
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BASE COUNT    3 a          3 c          9 g          2 t
ORIGIN
Query Match   62.2%; Score 11.2; DB 6; Length 17;
Best Local Similarity 66.8%; Pred. No. 2e+05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY            2 AUGGCCUACGCGCG 17
              1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db            2 AAGGCGATCGGTGCG 17
              1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 13
LOCUS         AX293459                      20 bp      DNA
DEFINITION    Sequence 5221 from Patent WO0179548.
ACCESSION     AX293459
VERSION       AX293459.1 GI:17055142
KEYWORDS
SOURCE        synthetic construct.
              artificial sequences.
REFERENCE
AUTHORS       Batanyi,F., Zilvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE         Method of designing addressable array for detection of nucleic acid
              sequence differences using ligase detection reaction
JOURNAL       Patent: WO 0179548-A 5221 25-OCT-2001;
              CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES      Location/Qualifiers
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              /db_xref="taxon:32630"
              /note="Hypothetical Probe Sequence"
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Best Local Similarity 71.4%; Pred. No. 3.4e+05;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY            2 AUGGCCUACGCGUG 15
              1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db            1 ACGGCGTACGGTG 14
              1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 14
LOCUS         AX189338                      18 bp      DNA
DEFINITION    Sequence 43 from Patent WO0148202.
ACCESSION     AX189338
VERSION       AX189338.1 GI:15142850
KEYWORDS
SOURCE        synthetic construct.
              synthetic construct.
              artificial sequences.
              1 (bases 1 to 18).
REFERENCE     Glover,D.M., Yamamoto,R. and Henderson,D.
AUTHORS       Mus101 and homologues thereof
TITLE         Patent: WO 0148202-A 43 05-JUL-2001;
JOURNAL       Cyclacel Limited (GB)
FEATURES      Location/Qualifiers
              1..18
SOURCE        /organism="synthetic construct"
              /db_xref="taxon:32630"

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GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen, Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:52:30 ; Search time 175.636 Seconds  
(Without alignments)  
230.795 Million cell updates/sec

Title: US-09-780-929-98

Sequence: 18  
1 aaugcccaucgugcgca 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 1367302

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	18	100.0	18	AA512348
2	12.8	71.1	20	AB15945
3	12.2	67.8	20	AB13941
4	11.8	65.6	20	AA94010
5	11.8	65.6	20	AA24197
6	11.8	65.6	20	AB13134
7	11.4	63.3	17	AA753656
8	11.4	63.3	17	AA753740
9	11.2	62.2	17	AA702004

10	11.2	62.2	17	AA239793
11	11.2	62.2	17	ABK00633
12	10.8	60.0	20	AB133501
13	10.6	58.9	18	ABD08688
14	10.6	58.9	18	ABD1065
15	10.6	58.9	20	AAV71835
16	10.6	58.9	20	AB13264
17	10.4	57.8	15	AA26286
18	10.4	57.8	20	ABN74903
19	10.4	57.8	20	AB193332
20	10.4	57.8	20	AB194339
21	10.2	56.7	15	AAV22883
22	10.2	56.7	15	AAV22883
23	10.2	56.7	17	AAV33065
24	10.2	56.7	17	AAV33066
25	10.2	56.7	17	AAV33067
26	10.2	56.7	17	AAV33068
27	10.2	56.7	17	ABK02662
28	10.2	56.7	18	AAV05734
29	10.2	56.7	18	AAV05734
30	10.2	56.7	18	AAV05734
31	10.2	56.7	19	AAV05734
32	10.2	56.7	20	AAV05734
33	10.2	56.7	20	AAV05734
34	10.2	56.7	20	AAV05734
35	10.2	56.7	20	AAV05734
36	10.2	56.7	20	AAV05734
37	10.2	56.7	20	AAV05734
38	10.2	56.7	20	AAV05734
39	10.2	56.7	20	AAV05734
40	10.2	56.7	20	AAV05734
41	10.2	56.7	20	AAV05734
42	10.2	56.7	20	AAV05734
43	10.2	56.7	20	AAV05734
44	10.2	56.7	20	AAV05734
45	10.2	56.7	20	AAV05734

#### ALIGNMENTS

RESULT 1

AA512348

21-NOV-2001 (first entry)

DNA encoding deoxyribozyme #8.

gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.

Synthetic.

WO200159102-A2.

16-AUG-2001.

08-FEB-2001; 2001WO-US04223.

08-FEB-2000; 2000US-0181360.

31-MAR-2000; 2000US-0193646.

(RIBO-) RIBOZYME PHARM INC.

(UTTA) UNIT YALE.

Breaker R, Belgelman L, Emilsson G.

WPI, 2001-536526/59.

New nucleic acids with endonuclease activity, such as ribozymes and

PT nucleozymes, for modulating gene expression in a plant, mammalian,  
PT bacterial or fungal cell -  
XX  
XX  
PS Claim 49; Page 77; 96pp; English.  
XX  
CC The invention relates to nucleic acid molecules with endonuclease  
CC activity, which are particularly useful for cleavage of RNA or DNA.  
CC The nucleic acids are used in a pharmaceutical composition and are used  
CC to modulate expression of a gene in a plant, mammalian, bacterial or  
CC fungal cell. They are used to cleave a separate nucleic acid, preferably  
CC RNA. The nucleic acids are used to inhibit gene expression and/or cell  
CC proliferation, and can be used to treat a disease or condition. More  
CC than one nucleic acid can be independently targeted to the same or  
CC different sites in a cell. The nucleic acids may be used to study DNA.  
CC The modifications to the nucleic acids optimises their catalytic activity  
CC and can maintain or enhance their activity. They exhibit a high degree  
CC of specificity for RNA. The present sequence represents the coding  
CC sequence of deoxyribozyme #8 used in the method of the invention.  
XX  
XX Sequence 18 BP; 4 A; 4 C; 6 G; 4 U; 0 other;  
SO  
Query Match 100.0%; Score 18; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
OY 1 AAUGGCCUAUCCGCGCGCA 18  
1 ||||||||||||||||  
Db 1 AAUGGCCUAUCCGCGCGCA 18  
ABIS95945  
RESULT 2  
ID ABIS95945  
XX ABIS95945 standard; DNA; 20 BP.  
XX  
XX ABIS95945;  
DT 16-FEB-2002 (first entry)  
XX  
DE Capture oligonucleotide Zip ID#3032 oligo #9.  
XX  
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;  
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;  
KW environmental monitoring; food industry; feed industry; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX WO200179548-A2.  
PN  
XX 25-OCT-2001.  
PD  
XX 04-APR-2001; 2001WO-US10958.  
PF  
XX 14-APR-2000; 2000US-197271P.  
PR  
XX (CORR ) CORNELL RES FOUND INC.  
PA  
XX Baranyi F, Zilvi M, Gerry NP, Favis R, Kloman R;  
PI  
XX WPI: 2002-034366/04.  
XX  
XX WPI: 2002-034366/04.  
XX  
PT Designing capture oligonucleotide probes for use on a support to which  
PT complementary oligonucleotides hybridize with little mismatch -  
XX  
XX Example 5; Fig 29; 300pp; English.  
XX  
XX The present invention describes a method (M1) for designing capture  
CC oligonucleotide probes (I) for use on a support to which complementary  
CC oligonucleotide probes (II) will hybridise with little mismatch, where  
CC (I) have melting temperatures within a narrow range. The method is useful  
CC for detecting infectious diseases caused by bacterial infectious agents  
CC e.g. salmonella, listeria monocytogenes and haemophilus influenza, fungal

```

CC infectious agents e.g. Cryptococcus neoformans; Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocyctotropic citrus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoviera volivulus, Entamoeba histolytica and Diacunculus
CC melnesiensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting complex scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
CC
SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 other:
Query Match 71.1%; Score 12.8; DB 24; Length 20;
Best Local Similarity 68.8%; Pred. NO. 7.2e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0
QY 2 AUGGCCUAGCGUGCG 17
   1 111 :1:111:111
Db      2 ACGGCTATACGGTCGC 17
RESULT 3
ABI93941
ID ABI93941 standard; DNA; 20 BP.
AC ABI93941;
XX
XX 16-FEB-2002 (first entry)
DT
DE Capture oligonucleotide zip ID#1028 Oligo #9.
XX
XX Human; K-Ras; PCR primer; probe; capture probe; mutation detection;
XX Liasse detection reaction; LDR; p53; BRCA1; BRCA2; Infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
OS Synthetic.
OS XX WO200179548-A2.
PN
XX 25-OCT-2001.
PD
XX 04-APR-2001; 2001WO-US10958.
PE
XX 14-APR-2000; 2000US-197271P.
PR
XX (CORR ) CORNELL RES FOUND INC.
PA
XX Barany F, Zilvi M, Gerry NP, Favis R, Kliman R;
PI
XX WPI, 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX Example 5; Fig 29; 30pp; English.
XX
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridise with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal

```

CC Infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
CC medineis. The method is also useful for detecting genetic diseases such  
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
CC involved in DNA amplification, replication, recombination or repair, the  
CC cancer is specifically associated with a gene selected from BRCA1 gene,  
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
CC method is also used for environmental monitoring, forensics and the food  
CC and feed industry, detecting comprises scanning (using e.g. a scanning  
CC electron microscope and infrared microscope) the support at the  
CC particular sites and identifying if ligation of the oligonucleotide probe  
CC sets occurred and correlating (using a computer) identified ligation to a  
CC presence or absence of the target nucleotide sequences. AB182074 to  
CC AB197546 represent oligonucleotide sequences used in the exemplification  
CC of the present invention.

CC XX Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 20;

Best Local Similarity 64.7%; Pred. No. 1.6e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 AUGGCCUAGCGGCGA 18

Db 3 ATGACCAATCGATCGCA 19

RESULT 4  
AA94010/c  
ID AA94010 standard; DNA: 20 BP.

AA94010;

DT 13-SEP-1999 (first entry)

PCR primer used to amplify an ORF of Chlamydia pneumoniae.

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;  
KW vaccine; neutralising epitope; PCR primer; ss.

Synthetic.  
Chlamydia pneumoniae.

MO9927105-A2.

PD 03-JUN-1999.

PF 20-NOV-1998; 98MO-IB01890.

PR 04-NOV-1998; 98US-0107078.

PR 21-NOV-1997; 97PR-0014673.

(GEST ) GENSET.

Griffais R;

WPI; 1999-357842/30.

Genome sequence of Chlamydia pneumoniae

Page 1636; Disclosure; 1912pp; English.

CC AAX91991-X97517 represent PCR primers used to amplify open reading  
CC frames and other nucleic acid sequences from the genome of  
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory  
CC disease such as pneumonia and bronchitis and is thought to be a  
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent  
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded  
CC by the open reading frames of the C. pneumoniae genome (see AAY34584-

CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors  
CC containing C. pneumoniae nucleotide sequences can also be used as  
CC immunogenic compositions, especially where the vector directs the  
CC expression of a neutralising epitope of C. pneumoniae.

CC XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;

Query Match 65.6%; Score 11.8; DB 20; Length 20;

Best Local Similarity 66.7%; Pred. No. 2.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AUGGCCUAGCGGUG 15

Db 20 AATGCCCTACGATG 6

RESULT 5  
AA244197/c  
ID AA244197 standard; DNA: 20 BP.

AA244197;

DT 24-MAR-2000 (first entry)

Murine cerebral nerve tissue differentiation DNA primer SAL.

Cerebral nerve tissue differentiation; murine; treatment; primer;  
KW cerebral nerve disease; ss.

Mus sp.

JP11318468-A.

PD 24-NOV-1999.

PF 15-MAY-1998; 98JP-0152027.

PR 15-MAY-1998; 98JP-0152027.

(KANA-) ZH KANAGAWA KAGAKU GIYUTSU ACAD.

(MEIRI) MEIRI MILK PROD CO LTD.

WPI; 2000-090527/08.

A new protein participating in the differentiation of cerebral nerve  
tissue cell - for the prevention and treatment of cerebral nerve tissue

Example 4; Page 13; 22pp; Japanese.

CC This invention describes a novel murine protein which is capable of  
CC inducing the differentiation of cerebral nerve tissue. The protein and  
CC the gene are expected to be used for the prevention and the treatment  
CC of cerebral nerve diseases. AA244193-244202 represent primers used in  
CC the isolation of the cerebral nerve tissue differentiation associated  
CC protein described in the method of the invention.

CC XX Sequence 20 BP; 7 A; 7 C; 4 G; 2 T; 0 other;

Query Match 65.6%; Score 11.8; DB 21; Length 20;

Best Local Similarity 60.0%; Pred. No. 2.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 UGCGCCUAGCGGUGCG 17

Db 20 TGGTCTCTCGTGGCG 6

RESULT 6  
AB193134  
ID AB193134 standard; DNA: 20 BP.  
XX AB193134;  
AC AB193134;  
XX

DT 15-FEB-2002 (first entry)  
 XX  
 DE Capture oligonucleotide zip ID#221 oligo #9.  
 XX  
 KM Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
 KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;  
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;  
 KM environmental monitoring; food industry; feed industry; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2001/9548-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 04-APR-2001; 2001WO-US10958.  
 XX  
 PR 14-APR-2000; 2000US-197271P.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;  
 XX  
 DR WPI; 2002-034366/04.  
 XX  
 PT Designing capture oligonucleotide probes for use on a support to which  
 XX complementary oligonucleotides hybridize with little mismatch -  
 XX  
 PS Example 5; Fig 29; 300pp; English.  
 XX  
 CS The present invention describes a method (M1) for designing capture  
 CC oligonucleotide probes (I) for use on a support to which complementary  
 CC oligonucleotide probes (II) will hybridize with little mismatch, where  
 CC (I) have melting temperatures within a narrow range. The method is useful  
 CC for detecting infectious diseases caused by bacterial infectious agents  
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal  
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Diacnulus  
 CC medinensis. The method is also useful for detecting genetic diseases  
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
 CC Detecting cancer involving Oncogenes, tumour suppressor genes, or genes  
 CC involved in DNA amplification, replication, recombination or repair. the  
 CC cancer is specifically associated with a gene selected from BRCA1 gene,  
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
 CC method is also used for environmental monitoring, forensics and the food  
 CC and feed industry, detecting comprises scanning (using e.g. a scanning  
 CC electron microscope and infrared microscope) the support at the  
 CC particular sites and identifying if ligation of the oligonucleotide probe  
 CC sets occurred and correlating (using a computer) identified ligation to a  
 CC presence or absence of the target nucleotide sequences. ABI82074 to  
 CC AB197546 represent oligonucleotide sequences used in the exemplification  
 CC of the present invention.  
 CC  
 XX  
 SO Sequence 20 BP; 1 A; 6 C; 6 G; 7 T; 0 other;  
 XX  
 Query Match 65.6%; Score 11.8; DB 24; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+03;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 OY 3 UGCGUACUGGUGCG 17  
 : |||:| |  
 Db 6 TGCCCTATCTGTGCG 20

RESULT 7  
 AAT53656  
 ID AAT53656 standard; RNA: 17 BP.  
 XX  
 AC AAT53656;  
 XX

DT 27-MAR-1997 (first entry)  
 XX  
 DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2341).  
 XX  
 KM Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KM gene expression; downregulation; Interleukin-5; IL-5; ICAM-1;  
 KM intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KM TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KM translocation; chronic myelogenous leukemia; CML; cancer;  
 KM Philadelphia chromosome; inflammation; autoimmune disease;  
 KM atherosclerosis; myocardial infarction; stroke; restenosis;  
 KM transplant rejection; rheumatoid arthritis; psoriasis;  
 KM myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KM human immunodeficiency virus; acquired immune deficiency syndrome;  
 KM AIDS; ss.  
 XX  
 OS Rattus rattus.  
 XX  
 PN WO9523225-A2.  
 XX  
 PD 31-AUG-1995.  
 XX  
 PF 23-FEB-1995; 95WO-IB00156.  
 XX  
 PR 30-JAN-1995; 95US-0380734.  
 XX  
 PR 23-FEB-1994; 94US-0201109.  
 PR 29-MAR-1994; 94US-0218934.  
 PR 04-APR-1994; 94US-0222795.  
 PR 07-APR-1994; 94US-0224483.  
 PR 15-APR-1994; 94US-0227958.  
 PR 15-APR-1994; 94US-0228041.  
 PR 18-MAY-1994; 94US-0245736.  
 PR 06-JUL-1994; 94US-0271280.  
 PR 15-AUG-1994; 94US-0291932.  
 PR 16-AUG-1994; 94US-0291433.  
 PR 17-AUG-1994; 94US-0292620.  
 PR 19-AUG-1994; 94US-0293520.  
 PR 02-SEP-1994; 94US-0300000.  
 PR 08-SEP-1994; 94US-0303039.  
 PR 23-SEP-1994; 94US-0311486.  
 PR 23-SEP-1994; 94US-0311749.  
 PR 28-SEP-1994; 94US-0314397.  
 PR 03-OCT-1994; 94US-0316771.  
 PR 07-OCT-1994; 94US-0319492.  
 PR 11-OCT-1994; 94US-0321993.  
 PR 04-NOV-1994; 94US-0334847.  
 PR 10-NOV-1994; 94US-0327608.  
 PR 28-NOV-1994; 94US-0345516.  
 PR 16-DEC-1994; 94US-0357577.  
 PR 23-DEC-1994; 94US-0363233.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J;  
 PI McSwiggan JA, Modak A, Pavco P, Beigelman L, Sullivan SM,  
 PI Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE,  
 PI Woolf T;  
 XX  
 DR WPI; 1995-351090/45.  
 XX  
 PT Ribozymes having modified bases and methods for producing them  
 XX for use in inhibiting disease related genes  
 XX  
 PS Claim 2; Page 203; 407pp; English.  
 XX  
 CS The present sequence represents a preferred target sequence for  
 CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1  
 CC mRNA at the nucleotide base position indicated in the DE line.  
 CC Regions of the mRNA that do not form secondary folding  
 CC structures and that contain potential hammerhead and hairpin  
 CC ribozyme cleavage sites were identified by computer analysis.  
 CC Ribozymes directed against these mRNA sequences were designed and



PS Claim 37: Page 62; 164pp; English.  
XX  
CC The present invention relates to enzymatic and antisense nucleic acid  
CC molecules that act as inhibitors of the expression of repressor genes  
CC encoding the T12 Orphan receptor, ESR3/COP-1, the GATA  
CC transcription factor gene, IRF-2 and/or the CAAAT Displacement  
CC Protein (CDP). Inhibition of the repressors removes prevents  
CC inhibition (and consequently increases expression of) genes involved in  
CC the production of erythropoietin, granulocyte colony stimulating factor  
CC protein and interferon alpha.  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 other;  
XX  
QY Query Match 62.2%; Score 11.2; DB 21; Length 17;  
Best Local Similarity 62.5%; Pred. No. 6.1e+03;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
XX  
Db 3 UGCGCCUAGCGUGCGA 18  
16 TGGCCCAATAGGTGCCA 1  
XX  
RESULT 10  
AAZ39793  
ID AAZ39793 standard; DNA; 17 BP.  
XX  
AC AAZ39793;  
XX  
DT 06-MAR-2000 (first entry)  
XX  
DE M13mpl8 ssDNA amplifying primer B1.  
XX  
KM Nucleic acid analysis; mass spectrometry; chemical compound analysis;  
KM PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9960007-A2.  
XX  
PD 25-NOV-1999.  
XX  
PF 17-MAY-1999; 99MO-GB01561.  
XX  
PR 15-MAY-1998; 98EP-0303873.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX  
PI Southern EM, Shchepilov MS, Housby JN, Hamilton AL, Elder JK;  
XX  
DR WPI; 2000-062435/05.  
XX  
PT Analysis of compounds using a solid support, labeled compounds and mass  
PT spectrometry  
XX  
PS Example 3: Page 26; 65pp; English.  
XX  
CC The invention provides new methods for the analysis of compounds,  
CC particularly nucleic acids, that use a solid support, labeled compounds  
CC and mass spectrometry. A novel method of making a set of labeled  
CC compounds, using of a support and a set of labels, comprises: (1) at  
CC least one first or intermediate step comprising dividing the support into  
CC lots, performing a different chemical reaction on each lot of the support  
CC so as either to modify that lot of the support or to couple a chemical  
CC moiety to that lot of the support, tagging a fraction of each lot of the  
CC moiety with a different label, and combining the lots of the support,  
CC and (2) at least one intermediate or final step comprising dividing the  
CC support into lots, performing a different chemical reaction on each lot  
CC of the support, so as either to modify that lot of the support or to  
CC couple a chemical moiety to that lot of the support, tagging a fraction  
CC of each lot of the support with a different label, where each different  
CC label is linked to a chemical moiety a labeled compound which is  
CC separable from the support, and combining the lots of the support. The  
CC methods and products are used for the analysis of chemical compounds,

CC particularly nucleic acid molecules.  
XX  
SQ Sequence 17 BP; 3 A; 3 C; 9 G; 2 T; 0 other;  
XX  
QY Query Match 62.2%; Score 11.2; DB 21; Length 17;  
Best Local Similarity 68.8%; Pred. No. 6.1e+03;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
XX  
Db 2 AUGGCCUAGCGUGCG 17  
1 AAGGCGCATCGGTGCG 16  
XX  
RESULT 11  
ABK00633/c  
ID ABK00633 standard; RNA; 17 BP.  
XX  
AC ABK00633;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human NCOGO Hammerhead Ribozyme #633.  
XX  
KM Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
KM muscular; CD20; neurite growth inhibitor gene; NCOGO; hammerhead ribozyme;  
KM DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
KM inflammatory arthropathy; central nervous system injury;  
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KM Parkinson's disease; ataxia; Huntington's disease;  
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
PN WO200159103-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001MO-US04273.  
XX  
PR 11-FEB-2000; 2000US-181797P.  
PR 28-FEB-2000; 2000US-185516P.  
PR 06-MAR-2000; 2000US-187128P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX  
PI Blatt L, MCSwigen J, Chowrira BW;  
XX  
DR WPI; 2001-607195/69.  
XX  
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,  
PT and central nervous system injury  
XX  
PS Claim 88: Page 76; 200pp; English.  
XX  
CC The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NCOGO).  
CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN  
CC motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinzyme  
CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used



PS Example 5; Fig 29; 300pp; English

CC Drosophila mus101 genomic and partial cDNAs. The mus101 is a member of



GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:32:43 ; Search time 1311.82 seconds  
(without alignments)  
222.225 Million cell updates/sec

Title: US-09-780-929-98

Sequence: 1 aaugcccauagugugcga 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 5800

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	9.6	53.3	20	17	AZ514794
C 2	9.2	51.1	20	17	AZ601483
C 3	8.4	46.7	15	14	BO511821
C 4	8.2	45.6	19	17	AZ329706
C 5	8.2	45.6	19	17	AZ515014
C 6	8.2	44.4	20	12	BF966452

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AZ514794	LOCUS	1M0361C13R Mouse 10kb plasmid UGCCIM library Mus musculus genomic clone UGCCIM0361C13 R, DNA sequence.	AZ514794					1 (bases 1 to 20)	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00

## ALIGNMENTS

Alignment 1	Alignment 2	Alignment 3	Alignment 4	Alignment 5	Alignment 6	Alignment 7	Alignment 8	Alignment 9	Alignment 10	Alignment 11	Alignment 12	Alignment 13	Alignment 14	Alignment 15	Alignment 16	Alignment 17	Alignment 18	Alignment 19	Alignment 20	Alignment 21	Alignment 22	Alignment 23	Alignment 24	Alignment 25	Alignment 26	Alignment 27	Alignment 28	Alignment 29	Alignment 30	Alignment 31	Alignment 32	Alignment 33	Alignment 34	Alignment 35	Alignment 36	Alignment 37	Alignment 38	Alignment 39	Alignment 40	Alignment 41	Alignment 42	Alignment 43	Alignment 44	Alignment 45
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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1																																												

Plate: 0361 row: C column: 13  
 Seq primer: CACACAGCAACAGCTATACCC  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers  
 1..20

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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0361C13"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, P1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN

Query Match 53.3%; Score 9.6; DB 17; Length 20;  
 Best Local Similarity 56.2%; Pred. No. 6.6e+05;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Oy 2 AUGGCCAUGCUGCG 17  
 1:|||||:11:11  
 Db 17 ATGGCCACTGTGCTGC 2

RESULT 2  
 AZ601483 20 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0419H15R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
 DEFINITION clone UUCG1M0419H15 R, DNA sequence.  
 ACCESSION AZ601483  
 VERSION AZ601483.1 GI:11723673  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

Plate: 0419 row: H column: 15  
 Seq primer: CACACAGCAACAGCTATACCC  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers  
 1..20

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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG1M0419H15"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, P1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN

Query Match 51.1%; Score 9.2; DB 17; Length 20;  
 Best Local Similarity 64.3%; Pred. No. 1e+06;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Oy 3 UGGCCAUCCGUGC 16  
 1:|||||11:11  
 Db 19 TGGCCCACTGTGC 6

RESULT 3  
 B0511821 15 bp mRNA linear EST 10-JUN-2002  
 LOCUS EST619236 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMH018 5' end, mRNA sequence.  
 ACCESSION B0511821  
 VERSION B0511821.1 GI:21370690  
 KEYWORDS EST.  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 15)  
 Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karayancheva,S.A.  
 Generation of a set of potato cDNA clones for microarray analyses  
 Unpublished (2002)  
 Other\_ESTs: EST619237  
 Contact: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Email: potato@tigr.org  
 This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or cdna@resgen.com  
 Seq primer: T3.

FEATURES  
source  
Location/Qualifiers  
1. 15  
/organism="Solanium tuberosum"  
/cultivar="Kennebec Or Bintje"  
/db\_xref="taxon:4113"  
/clone="STMH018"  
/clone\_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"  
/tissue\_type="mixed tissues"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site1: EcoRI; Site2: XhoI; supplier: Combination of untreated and phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."  
BASE COUNT  
ORIGIN  
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Query Match  
Best Local Similarity 46.7%; Score 8.4; DB 14; Length 15;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AAUGGCCUAD 10  
|||||:  
DB 5 AATGGCTCT 14  
RESULT 4  
AZ329706/c 19 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0054D06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0054D06 R, DNA sequence.  
ACCESSION AZ329706  
VERSION AZ329706.1 GI:10390686  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
TITLE  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0054 row: D column: 06  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0054D06"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (91473211419b/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
BASE COUNT  
ORIGIN  
5 a 7 c 2 g 5 t  
Query Match  
Best Local Similarity 45.6%; Score 8.2; DB 17; Length 19;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 4 GGCCUAGCGGCGC 16  
|||||:  
DB 17 GGCAATATAGGGGC 5  
RESULT 5  
AZ515014/c 19 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0054D06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0054D06 F, DNA sequence.  
ACCESSION AZ515014  
VERSION AZ515014.1 GI:10696330  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
TITLE  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0054 row: D column: 06  
Seq primer: CGTGTAAACGACGGCCACT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0054D06"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA



Db 12 GGCTTCCTT 2

RESULT 8  
LOCUS BM396285  
DEFINITION BM396285 18 bp mRNA linear EST 17-JAN-2002  
5009-0-2-A10.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM396285  
VERSION BM396285.1 GI:18196338  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila.  
ORGANISM Tetrahymena thermophila.  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 18)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.,  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
CONTACT: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
SOURCE location/Qualifiers  
1..18  
/organism="Tetrahymena thermophila"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript SK<sup>+</sup>. Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 3 a 3 c 8 g 4 t  
ORIGIN

Query Match 43.3%; Score 7.8; DB 13; Length 18;  
Best Local Similarity 54.5%; Pred. No. 4.8e+06;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 3 UGCGCUAUGCG 13  
|||||:|:|  
Db 8 TGGCTTATGCG 18

RESULT 9  
LOCUS A2787588  
DEFINITION A2787588 19 bp DNA linear GSS 16-FEB-2001  
2M0034A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0034A07 F, DNA sequence.

ACCESSION A2787588  
VERSION A2787588.1 GI:12926529  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

JOURNAL COMMENT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0034 Row: A Column: 07  
Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
SOURCE location/Qualifiers  
1..19  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="UUGC2M0034A07"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (911473114|9b|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 10 a 3 c 5 g 1 t  
ORIGIN

Query Match 43.3%; Score 7.8; DB 17; Length 19;  
Best Local Similarity 54.5%; Pred. No. 4.8e+06;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 4 GGCCUAGCGU 14  
|||||:|:|  
Db 17 GGCTATTGTT 7

RESULT 10  
LOCUS A2800646  
DEFINITION A2800646 19 bp DNA linear GSS 16-FEB-2001  
2M0058H14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0058H14 R, DNA sequence.

ACCESSION A2800646  
VERSION A2800646.1 GI:12952969  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

JOURNAL COMMENT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0038 row: H column: 14  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1.19  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U9GC2M0058H14"  
 /clone\_1ib="Mouse 10kb plasmid U9GCM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 3 a 4 c 7 g 5 t

Query Match 43.3%; Score 7.8; DB 17; Length 19;  
 Best Local Similarity 63.6%; Pred. No. 4.8e+06;  
 Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 GGCCUAGCGU 14  
 Db 5 GGCCCATTTGGT 15

RESULT 11  
 A2779244/c 20 bp DNA linear GSS 16-FEB-2001  
 LOCUS 2M001511F Mouse 10kb plasmid U9GCM library Mus musculus genomic  
 DEFINITION clone U9GC2M001511F, DNA sequence.  
 ACCESSION A2779244  
 VERSION A2779244.1 GI:12909701  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, R., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0015 row: I column: 19  
 Seq primer: CGTTGTAACAGCAGCCGACT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers  
 1.20  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U9GC2M0015119"  
 /clone\_1ib="Mouse 10kb plasmid U9GCM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 9 a 3 c 6 g 2 t

Query Match 43.3%; Score 7.8; DB 17; Length 20;  
 Best Local Similarity 54.5%; Pred. No. 4.9e+06;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AAUCCUAGC 11  
 Db 18 AGTGTCTCTATC 8

RESULT 12  
 HSMC21G06 20 bp DNA linear GSS 29-MAY-1997  
 LOCUS HSMC21G06  
 DEFINITION H.sapiens DNA for trapped exon (ID HMC21G06), genomic survey  
 ACCESSION X88286  
 VERSION X88286.1 GI:1437772  
 KEYWORDS GSS.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 20)  
 Chen, H.M., Rossier, C., Christ, R. and Antonarakis, S.E.  
 Cloning of trapped exons from human chromosome 21  
 Unpublished  
 2 (bases 1 to 20)  
 Antonarakis, S.E.  
 Direct Submission  
 Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of Medical Genetics, University and Cantonal Hospital of Geneva, CMU, 1 rue Michel-Servet, 1211 Geneva, SWITZERLAND  
 3 (bases 1 to 20)  
 Chen, H., Christ, R., Rossier, C., Morris, M.A., Lalloi, M.D. and



Antonarakis, S.E.  
Cloning of 539 potential exons of genes of human chromosome 21 by  
exon trapping  
JOURNAL Genome Res. 6 (8), 747-760 (1996)  
MEDLINE 97011340  
PUBMED 8858350

FEATURES  
SOURCE  
1. 20  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="21"  
1..20  
/note="trapped exon"

BASE COUNT 5 a 5 c 5 g 4 t 1 others  
ORIGIN

Query Match 43.3% Score 7.8; DB 17; Length 20;  
Best Local Similarity 58.3%; Pred. No. 4.9e+06;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 CUAGCGUGCGA 18  
1:1 1:1 1:1 1:1  
Db 4 CTACCGNMGTA 15

RESULT 13  
LOCUS BM394638 18 bp mRNA linear EST 17-JAN-2002  
DEFINITION 50072-2-5-B10.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
ACCESSION Tetrahymena thermophila cDNA, mRNA sequence.  
VERSION BM394638  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila.  
ORGANISM Tetrahymena thermophila.  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomata; Tetrahymenina; Tetrahymena.  
REFERENCE 1 (bases 1 to 18)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel  
, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
JOURNAL Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
FEATURES  
SOURCE  
1. 18  
/organism="Tetrahymena thermophila"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_id="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript SK-; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 3 a 3 c 10 g 2 t  
ORIGIN

Query Match 42.2% Score 7.6; DB 13; Length 18;  
Best Local Similarity 57.1%; Pred. No. 6e+06;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AUGGCCUAGCGUG 15  
1:1 1:1 1:1 1:1  
Db 2 ATGGGACAGCGGTG 15

RESULT 14  
ACCESSION AA885697

LOCUS AA885697 19 bp mRNA linear EST 09-JUN-1998  
DEFINITION OJ34f01.s1 NCI-CGAP Lu5 Homo sapiens cDNA clone IMAGE:1500217 3',  
similar to TR:Q92842 Q92842 HOMOLOG OF YEAST UPF1. [1] ;, mRNA  
sequence.  
ACCESSION AA885697  
VERSION AA885697.1 GI:3000805  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 19)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
[www-bio.1nl.gov/bdrp/image/image.html](http://www-bio.1nl.gov/bdrp/image/image.html)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
[www-bio.1nl.gov/bdrp/image/image.html](http://www-bio.1nl.gov/bdrp/image/image.html)  
Insert Length: 691 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
FEATURES  
SOURCE  
1. 19  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1500217"  
/clone\_id="NCI-CGAP Lu5"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; 1st strand cDNA was prepared from  
neuroendocrine lung carcinoid, and was then primed with a  
Not I - oligo(dT) primer. Double-stranded cDNA was ligated  
to Eco RI adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified  
pT73 vector. Library is normalized. Library was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 5 a 4 c 6 g 4 t  
ORIGIN

Query Match 42.2% Score 7.6; DB 9; Length 19;  
Best Local Similarity 57.1%; Pred. No. 6e+06;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 AAUGGCCUAGCGU 14  
1:1 1:1 1:1 1:1  
Db 1 AATAGCCAGCGGTG 14

RESULT 15  
LOCUS A1625518 19 bp mRNA linear EST 22-APR-1999  
DEFINITION cy56d06.x1 NCI-CGAP-Ut2 Homo sapiens cDNA clone IMAGE:2283083 3',  
similar to TR:P93237 P93237 PROLINE-RICH PROTEIN PRP2 PRECURSOR,  
; contains MSRL1 t1 MSRL1 repetitive element ;, mRNA sequence.  
ACCESSION A1625518

VERSION A1625518.1 GI:4650449

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 19)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 19

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2283083"

/clone\_lib="NCI-CGAP\_Ut2"

/tissue\_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab\_host="DH10B"

/note="Organ: uterus; Vector: PCMV-SPORT6; Site\_1: Salt;

Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.85 Kb. Life Technologies catalog #:

11539-012"

BASE COUNT 7 a 11 c 1 g 0 t

ORIGIN

Query Match 42.2%; Score 7.6; DB 9; Length 19;

Best Local Similarity 50.0%; Pred. No. 6e+06;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4' GGCCTAUCGCGCG 17

11 : : 11:111

Db 19 GGGTTTGTGTCG 6

Search completed: May 22, 2003, 20:17:07.

Job time : 1317.82 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:55:07 ; Search time 38.7273 seconds  
(without alignments)  
142.540 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18  
Sequence: 1 aaugcccaucgugcgca 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 247290

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.4	63.3	17	2	US-08-292-620A-1886 Sequence 1886, Ap
2	11.4	63.3	17	2	US-08-292-620A-1977 Sequence 1886, Ap
3	11.4	63.3	17	3	US-09-071-845-1886 Sequence 1886, Ap
4	11.4	63.3	17	3	US-09-071-845-1977 Sequence 1977, Ap
5	10.6	58.9	20	2	US-08-418-071-6 Sequence 6, Appli
6	10.4	57.8	15	1	US-08-182-968A-497 Sequence 497, App
7	10.4	57.8	15	2	US-08-774-306A-497 Sequence 497, App
8	10.4	57.8	15	3	US-09-064-156A-497 Sequence 497, App
9	10.2	56.7	17	4	US-09-059-779-5 Sequence 5, Appli
10	10.2	56.7	17	4	US-08-584-040-5815 Sequence 5815, Ap
11	10.2	56.7	17	4	US-08-584-040-5816 Sequence 5816, Ap
12	10.2	56.7	17	4	US-08-584-040-5817 Sequence 5817, Ap
13	10.2	56.7	18	2	US-09-108-837-3 Sequence 3, Appli
14	10	55.6	12	3	US-08-948-097-7 Sequence 7, Appli
15	10	55.6	20	1	US-08-222-177A-108 Sequence 108, App
16	9.8	54.4	16	3	US-08-872-917-11 Sequence 11, Appl
17	9.8	54.4	17	4	US-08-584-040-5814 Sequence 5814, Ap
18	9.8	54.4	20	2	US-08-837-201C-66 Sequence 66, Appl
19	9.8	54.4	20	4	US-09-364-416-66 Sequence 66, Appl
20	9.6	53.3	17	4	US-08-584-040-7863 Sequence 7863, Ap
21	9.6	53.3	17	4	US-08-679-645-264 Sequence 264, App
22	9.6	53.3	18	3	US-09-143-212-60 Sequence 60, Appl
23	9.6	53.3	18	4	US-08-679-645-643 Sequence 643, App
24	9.6	53.3	19	1	US-07-794-400-16 Sequence 16, Appl
25	9.6	53.3	19	1	US-08-397-470-16 Sequence 16, Appl
26	9.6	53.3	20	1	US-08-356-405-11 Sequence 11, Appl
27	9.6	53.3	20	2	US-08-478-178A-66 Sequence 66, Appl

C 28	9.6	53.3	20	2	US-08-488-177-66 Sequence 66, Appl
C 29	9.6	53.3	20	2	US-08-481-072A-66 Sequence 66, Appl
C 30	9.6	53.3	20	2	US-08-664-336-66 Sequence 66, Appl
C 31	9.6	53.3	20	2	US-08-481-066A-66 Sequence 66, Appl
C 32	9.6	53.3	20	4	US-09-313-930-6 Sequence 6, Appli
C 33	9.6	53.3	20	4	US-08-943-731-546 Sequence 546, App
C 34	9.6	53.3	20	4	US-09-593-589-72 Sequence 72, Appl
C 35	9.6	53.3	12	4	US-08-829-637A-66 Sequence 66, Appl
C 36	9.4	52.2	12	4	US-09-281-418-54 Sequence 54, Appl
C 37	9.4	52.2	18	1	US-08-126-564A-30 Sequence 30, Appl
C 38	9.4	52.2	18	2	US-08-465-380-100 Sequence 100, App
C 39	9.4	52.2	18	2	US-08-480-478-13 Sequence 13, Appl
C 40	9.4	52.2	18	2	US-08-486-397-100 Sequence 100, App
C 41	9.4	52.2	18	2	US-08-486-399-100 Sequence 100, App
C 42	9.4	52.2	18	2	US-08-461-965-100 Sequence 100, App
C 43	9.4	52.2	18	2	US-08-326-110A-13 Sequence 13, Appl
C 44	9.4	52.2	18	2	US-08-634-641-100 Sequence 100, App
C 45	9.4	52.2	18	3	US-09-249-471-100 Sequence 100, App

## ALIGNMENTS

RESULT 1  
US-08-292-620A-1886  
Sequence 1886, Application US/08292620A

Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: INTRACELLULAR ADHESION

TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A

FILING DATE: August 17, 1994

CLASSIFICATION: 435

Prior Application DATA:

Prior Application DATA: including application

Prior Application DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/149

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1886:

two

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-1886

Query Match 63.3%; Score 11.4; DB 2; Length 17;  
Best Local Similarity 92.3%; Pred. No. 7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCTAUCGGUGC 16  
||||| |||||  
DB 2 GGCCUGCGGUGC 14

## RESULT 2

US-08-292-620A-1977  
Sequence 1977, Application US/08292620A  
Patent No. 5837542

## GENERAL INFORMATION:

APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

two

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 1977:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-1977

Query Match 63.3%; Score 11.4; DB 2; Length 17;  
Best Local Similarity 92.3%; Pred. No. 7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCTAUCGGUGC 16  
||||| |||||  
DB 2 GGCCUGCGGUGC 14

## RESULT 3

US-09-071-845-1886  
Sequence 1886, Application US/09071845  
Patent No. 6132967

## GENERAL INFORMATION:

APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:

## CLASSIFICATION:

PRIOR APPLICATION DATA: including application  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 1886:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1886

Query Match 63.3%; Score 11.4; DB 3; Length 17;  
Best Local Similarity 92.3%; Pred. No. 7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCTAUCGGUGC 16  
||||| |||||  
DB 2 GGCCUGCGGUGC 14

```
RESULT 4
US-09-071-845-1977
; Sequence 1977, Application US/09071845
; Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Diaper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 1977:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1977

Query Match      63.3%; Score 11.4; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. No. 7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GGGCUAUGGUGC 16
DB      2 GGGCUGGUGGUGC 14

RESULT 5
US-08-418-071-6
; Sequence 6, Application US/08418071
; Patent No. 5846705
GENERAL INFORMATION:
APPLICANT: Wu, Rey-Yuh
APPLICANT: You, Li-Ru
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF TWO CIRCULAR ssDNA
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AND METHOD FOR DETE
TITLE OF INVENTION: BANANA BUNCHY TOP VIRUS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,071
FILING DATE: 06-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: DCB-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc="Oligonucleotide primer BB-1"
ANTI-SENSE: YES
US-08-418-071-6

Query Match      58.9%; Score 10.6; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 AUGCCUAGGUGCGA 18
DB      2 AUGGCTATCGAGCGCA 18

RESULT 6
US-08-182-968A-497/C
; Sequence 497, Application US/08182968A
; Patent No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
```

SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 497:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-497  
Query Match  
Best Local Similarity 57.8%; Score 10.4; DB 1; Length 15;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 2 AUGGCCUACGG 13  
Db 14 ATGGCCTATTGG 3  
RESULT 7  
US-08-774-306A-497/c  
Sequence 497, Application US/08774306A  
Patent No. 5869253  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
City: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,306A  
FILING DATE: December 26, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 497:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-306A-497  
Query Match  
Best Local Similarity 57.8%; Score 10.4; DB 2; Length 15;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 2 AUGGCCUACGG 13  
Db 14 ATGGCCTATTGG 3  
RESULT 8  
US-09-064-156A-497/c  
Sequence 497, Application US/09064156A  
Patent No. 6132966  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 498  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
City: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/064,156A  
FILING DATE: April 21, 1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/774,306  
FILING DATE: December 26, 1996  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 234/083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 497:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-064-156A-497  
Query Match  
Best Local Similarity 57.8%; Score 10.4; DB 3; Length 15;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 2 AUGGCCUACGG 13  
Db 14 ATGGCCTATTGG 3

RESULT 9  
US-09-059-779-5  
; Sequence 5, Application US/09059779  
; Patent No. 6153743  
; GENERAL INFORMATION:  
; APPLICANT: Hubbell Earl A.  
; APPLICANT: Lubert Stryer  
; APPLICANT: Michael P. Miltmann  
; TITLE OF INVENTION: Lithographic Mask Design and  
; TITLE OF INVENTION: Synthesis of Diverse Probes on a Substrate  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rilter, Van Pelt & Yi LLP  
; STREET: 4906 El Camino Real, Suite 205  
; CITY: Los Altos  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,779  
; FILING DATE: April 13, 1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rilter, Michael J.  
; REGISTRATION NUMBER: 36,653  
; REFERENCE/DOCKET NUMBER: AFTYP015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-903-3500  
; TELEFAX: 650-903-3501  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (oligonucleotide)  
; US-09-059-779-5

Query Match 56.7%; Score 10.2; DB 3; Length 15;  
Best Local Similarity 60.0%; Pred. No. 3.4e+03;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGGCCUAGCGGUGC 16  
||| ||| ||| |||  
Db 1 ATGGCAGATCGATGC 15

RESULT 10  
US-08-584-040-5815  
; Sequence 5815, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700

CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5815:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-5815

Query Match 56.7%; Score 10.2; DB 4; Length 17;  
Best Local Similarity 80.0%; Pred. No. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 UGGCCUAGCGGUGC 17  
||| ||| ||| ||| |||  
Db 3 UGGUCUUGCGGUGC 17

RESULT 11  
US-08-584-040-5816  
; Sequence 5816, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5816:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-5816

Query Match 56.7%; Score 10.2; DB 4; Length 17;  
Best Local Similarity 80.0%; Pred. No. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 UGCGCUAUCGUGCG 17  
||| || ||||| |  
Db 2 UGUCUUCUGGUGUG 16

RESULT 12  
US-08-584-040-5817  
Sequence 5817, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5817:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-5817

Query Match 56.7%; Score 10.2; DB 4; Length 17;  
Best Local Similarity 80.0%; Pred. No. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 UGCGCUAUCGUGCG 17  
||| || ||||| |  
Db 1 UGUCUUCUGGUGUG 15

RESULT 13  
US-09-108-837-3  
Sequence 3, Application US/09108837  
Patent No. 5972617  
GENERAL INFORMATION:  
APPLICANT: SAMI, Manabu  
TITLE OF INVENTION: OLIGONUCLEOTIDE FOR DETECTING LACTIC ACID BACTERIA AND  
FILE REFERENCE: SAMI  
CURRENT APPLICATION NUMBER: US/09/108,837  
CURRENT FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: 09-195268  
EARLIER FILING DATE: 1997-07-07  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Lactobacillus brevis  
US-09-108-837-3

Query Match 56.7%; Score 10.2; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 3.5e+03;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGCCUAUCGUG 15  
||: ||| :||| :|  
Db 1 AAUGCCAAATCGTG 15

RESULT 14  
US-08-948-097-7  
Sequence 7, Application US/08948097C  
Patent No. 6103493  
GENERAL INFORMATION:  
APPLICANT: Skerra, Arne  
APPLICANT: Voss, Selma  
TITLE OF INVENTION: Streptavidin Mutains  
FILE REFERENCE: HDR 1119  
CURRENT APPLICATION NUMBER: US/08/948,097C  
CURRENT FILING DATE: 1997-10-09  
EARLIER APPLICATION NUMBER: DE 196 41 876.3  
EARLIER FILING DATE: 1996-10-10  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO 7  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: CDS  
OTHER INFORMATION: Synthesized  
US-08-948-097-7

Query Match 55.6%; Score 10; DB 3; Length 12;  
Best Local Similarity 80.0%; Pred. No. 4.4e+03;



Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 AUGGUGCGA 18  
1111111111

Db 1 ATGGGTGCGA 10

## RESULT 15

US-08-222-177A-108/c  
Sequence 108, Application US/08222177A  
Patent No. 5582979

GENERAL INFORMATION:

APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:

ADDRESSEE: Demitt Ross & Stevens, S.C.

STREET: 8000 Excelstior Drive, Suite 401

CITY: Madison

STATE: Wisconsin

COUNTRY: USA

ZIP: 53717-1914

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/222,177A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/341,562

FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,492

REFERENCE/DOCKET NUMBER: 09865, 601

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 831-2100

TELEFAX: (608) 831-2106

TELEX:

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: mfd19p1

US-08-222-177A-108

Query Match 55.6%; Score 10; DB 1; Length 20;

Best Local Similarity 61.1%; Pred. No. 4.7e+03;

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AUGGCUUUCGUGCGA 18  
11111111111111111111

Db 18 AATGGCCAAAGGGTTAGA 1

Search completed: May 22, 2003, 20:18:25

Job time : 40.7273 secs

GenCore version 5.1.4-P5-4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:36:48 ; Search time 95.0909 Seconds  
(without alignments)  
279.329 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18

Sequence: 1 aaugccuauccgugcgca 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 191488

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

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2: /cgn2_6/ptodata/1/pubpna/PTI_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCYUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	10	US-09-780-929-98
2	11.2	62.2	17	9	US-09-780-533A-633
3	11.2	62.2	19	9	US-09-796-081-3
4	11.2	62.2	19	9	US-09-796-081-4
5	10.4	57.8	15	10	US-09-504-231A-519
6	10.4	57.8	15	10	US-09-274-553D-519
7	10.4	57.8	18	10	US-09-969-373-3464
8	10.4	57.8	20	9	US-10-068-160-36
9	10.2	56.7	17	9	US-09-780-533A-2600
10	10.2	56.7	17	9	US-09-780-533A-2602
11	10.2	56.7	18	10	US-09-969-373-2070
12	10	55.6	18	9	US-09-961-700A-29
13	10	55.6	20	9	US-09-232-785-373
14	9.8	54.4	17	9	US-09-825-805-737
15	9.6	53.3	17	9	US-09-825-805-712
16	9.6	53.3	17	9	US-09-848-754A-1942
17	9.6	53.3	17	9	US-09-848-754A-1942
18	9.6	53.3	17	9	US-09-848-754A-3017
19	9.6	53.3	18	9	US-09-961-077-643

## ALIGNMENTS

20	9.6	53.3	18	9	US-10-132-652-18	Sequence 18, Appl
21	9.6	53.3	20	10	US-09-766-399-17	Sequence 17, Appl
22	9.4	52.2	17	9	US-09-877-478-300	Sequence 300, App
23	9.4	52.2	17	9	US-09-877-478-988	Sequence 988, App
24	9.4	52.2	17	9	US-09-877-478-989	Sequence 989, App
25	9.4	52.2	17	9	US-09-877-478-1719	Sequence 1719, App
26	9.4	52.2	17	9	US-09-877-478-1967	Sequence 1967, App
27	9.4	52.2	17	9	US-09-877-478-2309	Sequence 2309, App
28	9.4	52.2	18	10	US-09-969-373-2727	Sequence 2727, App
29	9.4	52.2	18	10	US-09-969-373-2729	Sequence 2729, App
30	9.4	52.2	18	10	US-09-969-373-3465	Sequence 3465, App
31	9.4	52.2	18	10	US-09-969-373-4573	Sequence 4573, App
32	9.4	52.2	19	9	US-10-080-959A-3	Sequence 3, Appl1
33	9.4	52.2	20	9	US-09-924-981-5	Sequence 12, Appl
34	9.4	52.2	20	10	US-10-267-117-12	Sequence 135, App
35	9.2	51.1	15	10	US-09-504-231A-135	Sequence 135, App
36	9.2	51.1	15	10	US-09-274-553D-135	Sequence 2601, App
37	9.2	51.1	17	9	US-09-780-533A-2301	Sequence 2601, App
38	9.2	51.1	17	9	US-09-780-533A-2661	Sequence 620, App
39	9.2	51.1	17	9	US-09-848-754A-620	Sequence 9650, App
40	9.2	51.1	17	10	US-09-866-108-9650	Sequence 9651, App
41	9.2	51.1	17	10	US-09-866-108-9651	Sequence 9652, App
42	9.2	51.1	17	10	US-09-866-108-9652	Sequence 9653, App
43	9.2	51.1	17	10	US-09-866-108-9653	Sequence 211, App
44	9.2	51.1	18	9	US-09-961-700A-21	
45	9.2	51.1	18	9	US-09-747-377-211	

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RESULT 1
US-09-780-929-98
Sequence 98, Application US/09780929
Patent No. US20020151693A1
GENERAL INFORMATION:
APPLICANT: Breaker, Ronald
APPLICANT: Belgeiman, Leo
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MH800-884-H (500/001)
CURRENT APPLICATION NUMBER: US/09/780,929
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: US 60/181,360
PRIORITY FILING DATE: 2000-02-08
SOFTWARE: PatentIn version 3.0
SEQ ID NO 98
LENGTH: 18
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-929-98
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Query Match 100.0%; Score 18; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.87;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AAUGGCCUACGUGCGCA 18
Db 1 AAUGGCCUACGUGCGCA 18
```

```
RESULT 2
US-09-780-533A-633/C
Sequence 633, Application US/09780533A
Patent No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Chowitra, Bharat
```

APPLICANT: Haeblerl, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NCO Gene  
FILE REFERENCE: MBH800.878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780,533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181,797  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 633  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-780-533A-633

Query Match 62.2%; Score 11.2; DB 9; Length 17;  
Best Local Similarity 56.2%; Pred. No. 5.9e+03;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGGCCUAUCGUGC 16  
DB 16 AATGATCTATCTGTGC 1

RESULT 3  
US-09-796-081-3  
Sequence 3, Application US/09796081  
Publication No. US20030045538A1  
GENERAL INFORMATION:  
APPLICANT: Danaboyina, Ramalah  
APPLICANT: Nadukkudy, Varghese E.  
APPLICANT: Joshy, Joseph  
TITLE OF INVENTION: VILOGEN LINKED ACRIDINE BASED MOLECULE AND PROCESS FOR  
FILE REFERENCE: 3108/01342  
CURRENT APPLICATION NUMBER: US/09/796,081  
CURRENT FILING DATE: 2001-08-14  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-796-081-3

Query Match 62.2%; Score 11.2; DB 9; Length 19;  
Best Local Similarity 56.2%; Pred. No. 5.9e+03;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGGCCUAUCGUGC 16  
DB 2 ACTGCGCTTTCGCTGC 17

RESULT 4  
US-09-796-081-4/C  
Sequence 4, Application US/09796081  
Publication No. US20030045538A1  
GENERAL INFORMATION:  
APPLICANT: Danaboyina, Ramalah  
APPLICANT: Nadukkudy, Varghese E.  
APPLICANT: Joshy, Joseph  
TITLE OF INVENTION: VILOGEN LINKED ACRIDINE BASED MOLECULE AND PROCESS FOR  
FILE REFERENCE: 3108/01342  
CURRENT APPLICATION NUMBER: US/09/796,081  
CURRENT FILING DATE: 2001-08-14  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 19

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-796-081-4

Query Match 62.2%; Score 11.2; DB 9; Length 19;  
Best Local Similarity 56.2%; Pred. No. 5.9e+03;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGGCCUAUCGUGC 16  
DB 18 ACTGCGCTTTCGCTGC 3

RESULT 5  
US-09-504-231A-519/C  
Sequence 519, Application US/09504231A  
Patent No. US20020013458A1  
GENERAL INFORMATION:  
APPLICANT: Blatt, Lawrence  
APPLICANT: McSwiggen, James  
APPLICANT: Roberts, Beth  
APPLICANT: Pavco, Pamela  
APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL  
FILE REFERENCE: tpi 247/282  
CURRENT APPLICATION NUMBER: US/09/504,231A  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 09/274,553  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3242  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 519  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-519

Query Match 57.8%; Score 10.4; DB 10; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.7e+04;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 AUGGCCUAUCG 13  
DB 14 AATGCGCTATTGC 3

RESULT 6  
US-09-274-553D-519/C  
Sequence 519, Application US/09274553D  
Patent No. US20020082225A1  
GENERAL INFORMATION:  
APPLICANT: Blatt, Lawrence  
APPLICANT: McSwiggen, James  
APPLICANT: Roberts, Beth  
APPLICANT: Pavco, Pamela  
APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL  
FILE REFERENCE: tpi 247/282  
CURRENT APPLICATION NUMBER: US/09/274,553D  
CURRENT FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608

PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3148  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 519  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553D-519

Query Match 57.8%; Score 10.4; DB 10; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.7e+04;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AUGGCCUAGCG 13  
DB 14 ATGGCCTATTGG 3

RESULT 7  
US-09-969-373-3464/c  
Sequence 3464, Application US/09969373  
Patent No. US20020133852A1  
GENERAL INFORMATION:  
APPLICANT: Effertz, Roger J.  
APPLICANT: Hauge, Brian M.  
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
FILE REFERENCE: 38-10(52679)A  
CURRENT APPLICATION NUMBER: US/09/969,373  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US 09/754,853  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 09/760,427  
PRIOR FILING DATE: 2001-01-13  
PRIOR APPLICATION NUMBER: US 09/855,768  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 4593  
SEQ ID NO 3464  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-969-373-3464

Query Match 57.8%; Score 10.4; DB 10; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.7e+04;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 CUAGCGUGCA 18  
DB 12 CTATCGTGGCA 1

RESULT 8  
US-10-068-160-36/c  
Sequence 36, Application US/10068160  
Publication No. US20030060440A1  
GENERAL INFORMATION:  
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE  
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES  
APPLICANT: KLIMMAN, Dennis  
APPLICANT: VERTHELYI, Daniela  
APPLICANT: ISHII, Ken  
TITLE OF INVENTION: OLIGODEXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE  
FILE REFERENCE: 4239-61999  
CURRENT APPLICATION NUMBER: US/10/068,160  
CURRENT FILING DATE: 2002-02-06  
PRIOR APPLICATION NUMBER: 60/128,898  
PRIOR FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 36  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide  
US-10-068-160-36

Query Match 57.8%; Score 10.4; DB 9; Length 20;  
Best Local Similarity 66.7%; Pred. No. 1.7e+04;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCUAGCGUGC 16  
DB 15 GCCTATCGATGC 4

RESULT 9  
US-09-780-533A-2300/c  
Sequence 2300, Application US/09780533A  
Publication No. US20030060611A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwiggen, Jim  
APPLICANT: Chowrira, Bharat  
APPLICANT: Haeblerli, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
FILE REFERENCE: MBH80,878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780,533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181,797  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2300  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-780-533A-2300

Query Match 56.7%; Score 10.2; DB 9; Length 17;  
Best Local Similarity 53.3%; Pred. No. 2.2e+04;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGGCCUAGCGUGC 16  
DB 17 ATGATCTATCTGTGC 3

RESULT 10  
US-09-780-533A-2662/c  
Sequence 2662, Application US/09780533A  
Publication No. US20030060611A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwiggen, Jim  
APPLICANT: Chowrira, Bharat  
APPLICANT: Haeblerli, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
FILE REFERENCE: MBH80,878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780,533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181,797  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2662  
LENGTH: 17  
TYPE: RNA

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; ORGANISM: Homo sapiens
US-09-780-533A-2662

Query Match
Best Local Similarity 56.7%; Score 10.2; DB 9; Length 17;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGGCCUAGCGUG 15
DB 15 AATGATCTATCTGTG 1

RESULT 11
US-09-969-373-2070
; Sequence 2070, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Eifert, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2070
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2070

Query Match
Best Local Similarity 56.7%; Score 10.2; DB 10; Length 18;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGGCCUAGCGUG 15
DB 4 AATGCCAATTCGTG 18

RESULT 12
US-09-961-700A-29
; Sequence 29, Application US/09961700A
; Publication No. US20020187482A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Zicai
; APPLICANT: Wang, Hong-Yan
; APPLICANT: Wahlestedt, Claes
; TITLE OF INVENTION: Methods and Means of RNA Analysis
; FILE REFERENCE: 13522-003001
; CURRENT APPLICATION NUMBER: US/09/961,700A
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 60/235,029
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
US-09-961-700A-29

Query Match
Best Local Similarity 55.6%; Score 10; DB 9; Length 18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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OY 1 AAUGGCCUAGCGUGCGA 18
DB 1 AATGGGCTTCTGTCTGA 18

RESULT 13
US-09-232-785-373/c
; Sequence 373, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
; APPLICANT: International Paper Co.
; APPLICANT: Echt, Craig. S
; APPLICANT: Nelson, C. Dana
; TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES
; FILE REFERENCE: 4481/1F18BUS1
; CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Pinus taeda L.
US-09-232-785-373

Query Match
Best Local Similarity 55.6%; Score 10; DB 9; Length 20;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 AAUGGCCUAGCGUGCGA 18
DB 18 AATGGTCTATCGACCGA 1

RESULT 14
US-09-825-805-737
; Sequence 737, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Beaudry, Leo
; APPLICANT: Belgelman, Leo
; APPLICANT: Karpelsky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Svedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucle
; FILE REFERENCE: MBH800-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 737
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
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GenCore version 5.1.4-P5-A578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:59:38 ; Search time 2074.36 Seconds  
(without alignments)  
218.170 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18

Sequence: 1 aaugccuacugugcga 18

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 1600790

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	18	100.0	18	30	US-09-780-929-98
2	12.2	67.8	20	31	US-09-827-383-650
3	12.2	67.8	20	31	US-09-827-383-803
4	12.2	67.8	20	31	US-09-827-383-803
5	12.2	67.8	20	31	US-09-827-383-803
6	11.8	65.6	16	1	PCT-US02-25943-8274
7	11.8	65.6	16	1	PCT-US02-25943-8274
8	11.8	65.6	16	1	PCT-US02-25943-8274
9	11.8	65.6	16	1	PCT-US02-25943-8274
10	11.8	65.6	16	1	PCT-US02-25943-8274
11	11.4	63.3	20	28	US-09-102-708-17627
12	11.4	63.3	20	28	US-09-102-708-17627
13	11.4	63.3	20	28	US-09-102-708-17627
14	11.2	62.2	17	21	US-09-546-745A-1992
15	11.2	62.2	17	21	US-09-546-745A-1992
16	11.2	62.2	19	30	US-09-796-081-4
17	11.2	62.2	19	30	US-09-796-081-4
18	11.2	62.2	20	43	US-10-262-666-77
19	10.8	60.0	15	1	PCT-US02-25940-16232
20	10.8	60.0	15	1	PCT-US02-25940-16232
21	10.8	60.0	15	1	PCT-US02-25942-1512

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22 10.8 60.0 15 1 PCT-US02-25942-1775 Sequence 1775, Ap
23 10.8 60.0 15 17 US-09-322-909-4 Sequence 4, Appl
24 10.8 60.0 15 17 US-10-227-563-16232 Sequence 16232, A
25 10.8 60.0 15 42 US-10-227-563-19783 Sequence 19783, A
26 10.8 60.0 15 42 US-10-227-567-1512 Sequence 1512, A
27 10.8 60.0 15 42 US-10-227-567-1775 Sequence 1775, Ap
28 10.8 60.0 20 7 US-08-341-469-10 Sequence 6, Appl
29 10.6 58.9 20 8 US-08-484-735-6 Sequence 11863, A
30 10.6 58.9 20 19 PCT-US01-05126-16 Sequence 16, Appl
31 10.4 57.8 15 11 US-08-774-306-497 Sequence 497, App
32 10.4 57.8 15 11 US-09-274-553-1054 Sequence 1054, App
33 10.4 57.8 15 16 US-09-274-553B-519 Sequence 519, App
34 10.4 57.8 15 16 US-09-274-553C-519 Sequence 519, App
35 10.4 57.8 15 16 US-09-274-553D-519 Sequence 519, App
36 10.4 57.8 15 16 US-09-504-231A-519 Sequence 519, App
37 10.4 57.8 15 19 US-09-504-231B-519 Sequence 519, App
38 10.4 57.8 15 19 US-09-504-231B-519 Sequence 519, App
39 10.4 57.8 15 23 US-09-611-931-519 Sequence 519, App
40 10.4 57.8 15 24 US-09-611-931A-519 Sequence 497, App
41 10.4 57.8 15 24 US-09-633-515-497 Sequence 26, Appl
42 10.4 57.8 16 28 US-08-705-400-26 Sequence 61, Appl
43 10.4 57.8 16 28 US-08-705-400-61 Sequence 26, Appl
44 10.4 57.8 16 30 US-09-765-400-26 Sequence 61, Appl
45 10.4 57.8 16 30 US-09-765-400-61

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## ALIGNMENTS

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RESULT 1
US-09-780-929-98
; Sequence 98, Application US/09780929
; GENERAL INFORMATION:

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; APPLICANT: Ribozyne Pharmaceuticals, Inc
; APPLICANT: Breakey, Ronald
; APPLICANT: Belgelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH800-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09/780, 929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 'Enzymatic Nucleic Acid
US-09-780-929-98

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Query Match 100.0%; Score 18; DB 30; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 AAUGGCCUAGCGGCGCA 18
Db 1 AAUGGCCUAGCGGCGCA 18

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RESULT 2
US-09-827-383-650/c
; Sequence 650, Application US/09827383
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Macdonald Morris
; APPLICANT: Tom Ryder
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays
; FILE REFERENCE: 3108
; CURRENT APPLICATION NUMBER: US/09/827,383

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; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/195,585
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 650
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-383-650

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```

Query Match 67.8%; Score 12.2; DB 31; Length 20;
Best Local Similarity 64.7%; Pred. No. 2e+04;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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```

OY 1 AAUGGCCUAGCGGCGC 17
Db 19 AATCGCTCTCGAGCG 3

```

```

RESULT 3
US-09-827-383-803
; Sequence 803, Application US/09827383
; GENERAL INFORMATION:

```

```

; APPLICANT: Michael Mittmann
; APPLICANT: Macdonald Morris
; APPLICANT: Tom Ryder
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays
; FILE REFERENCE: 3108
; CURRENT APPLICATION NUMBER: US/09/827,383
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/195,585
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 803
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-383-803

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Query Match 67.8%; Score 12.2; DB 31; Length 20;
Best Local Similarity 64.7%; Pred. No. 2e+04;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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```

OY 2 AUGGCCUAGCGGCGCA 18
Db 4 ATGCGCATCTCGTGGCA 20

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RESULT 4
US-09-827-383A-650/c
; Sequence 650, Application US/09827383A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Macdonald Morris
; APPLICANT: Tom Ryder
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays
; FILE REFERENCE: 3108
; CURRENT APPLICATION NUMBER: US/09/827,383A
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/195,585
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 650
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens

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LOCATION: (1820695)...(1820710)
OTHER INFORMATION: Chromosome - 1 Strand = positive ConnectonObjectNumber = 19657
US-10-227-565-18265

Query Match
Best Local Similarity 65.6%; Score 11.8; DB 42; Length 16;
File Reference: 38-10(15804)A
Mismatches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCCUACGCGCGA 18
    |||||:|:|:|
Db 2 GGCCTATCGCGCGA 16

RESULT 10
US-09-198-452A-3336/C
Sequence 3336, Application US/09198452A
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 3336
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3336

Query Match
Best Local Similarity 65.6%; Score 11.8; DB 15; Length 20;
File Reference: 38-10(15804)C
Mismatches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAUGCCUACGCGUG 15
    |||||:|:|:|
Db 20 AATGCTATCGATG 6

RESULT 11
US-09-703-708-17627
Sequence 17627, Application US/09703708
GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15804)C
CURRENT APPLICATION NUMBER: US/09/703,708
CURRENT FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/164,320
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/183,791
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 17627
LENGTH: 20
TYPE: DNA
ORGANISM: Xanthomonas campestris
US-09-703-708-17627

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 28; Length 20;
File Reference: 38-10(15804)A
Mismatches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGCGCUACGCGUG 15
    :|||:|:|:|
Db 2 TGGCCTATCTGTG 14

RESULT 12
US-60-164-320-17627
Sequence 17627, Application US/60164320
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GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15804)A
CURRENT APPLICATION NUMBER: US/60/164,320
CURRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 17627
LENGTH: 20
TYPE: DNA
ORGANISM: Xanthomonas campestris
US-60-164-320-17627

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 60; Length 20;
File Reference: 38-10(15804)A
Mismatches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGCGCUACGCGUG 15
    :|||:|:|:|
Db 2 TGGCCTATCTGTG 14

RESULT 13
US-60-183-791-17627
Sequence 17627, Application US/60183791
GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15804)B
CURRENT APPLICATION NUMBER: US/60/183,791
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 17627
LENGTH: 20
TYPE: DNA
ORGANISM: Xanthomonas campestris
US-60-183-791-17627

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 62; Length 20;
File Reference: 38-10(15804)A
Mismatches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGCGCUACGCGUG 15
    :|||:|:|:|
Db 2 TGGCCTATCTGTG 14

RESULT 14
US-09-546-745A-1992/C
Sequence 1992, Application US/09546745A
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Zwick, Michael
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
FILE REFERENCE: 237/193
CURRENT APPLICATION NUMBER: US/09/546,745A
CURRENT FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 7043
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1992
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-1992

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 21; Length 17;
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Best Local Similarity 62.5%; Pred. No. 7.8e+04;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 UGCGCUAUCGUGCA 18  
:|||||:|||||  
Db 16 TGCGCCATAGTGCCA 1

## RESULT 15

US-09-780-533A-633/C  
; Sequence 633, Application US/09780533A  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haebeli, Pete  
; TITLE OF INVENTION: Method and Reagent for the inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 633  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-633

Query Match 62.2%; Score 11.2; DB 30; Length 17;  
Best Local Similarity 56.2%; Pred. No. 7.8e+04;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Db 16 AATGATCTATCTGTGC 1

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Job time : 2076.36 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:04:38 ; Search time 445.636 Seconds

(without alignments)  
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Title: US-09-780-929-98

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Sequence: 1 aagccuacugcugcgca 18

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Searched: 6438716 seqs, 2593467500 residues

Total number of hits satisfying chosen parameters: 667140

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	11.4	63.3	18	9	US-10-259-273-36
5	10.8	60.0	15	8	US-10-367-892-16232
6	10.8	60.0	15	8	US-10-367-892-19783
7	10.8	60.0	15	8	US-10-303-778-1079
8	10.8	60.0	15	8	US-10-287-787-23056
9	10.8	60.0	16	8	US-10-287-787-23057
10	10.8	60.0	17	1	PCT-US03-10154-33
11	10.8	60.0	17	8	US-10-404-724-33
12	10.8	60.0	18	8	US-10-237-016A-39
13	10.8	60.0	18	9	US-10-217-106-47
14	10.8	60.0	18	9	US-10-237-016-39
15	10.8	60.0	19	8	US-10-287-787-16018
16	10.8	60.0	19	8	US-10-287-787-22109
17	10.8	60.0	20	6	US-09-827-383B-232
18	10.6	58.9	18	9	US-10-168-424-43
19	10.4	57.8	15	6	US-09-274-553E-519
20	10.4	57.8	15	8	US-10-287-787-12676
21	10.4	57.8	16	8	US-10-287-787-142
22	10.4	57.8	16	8	US-10-287-787-6051

C 23	10.4	57.8	16	8	US-10-287-787-20529	Sequence 20529, A
C 24	10.4	57.8	16	8	US-10-287-787-26977	Sequence 26977, A
C 25	10.4	57.8	17	9	US-10-084-839-3310	Sequence 3310, Ap
C 26	10.4	57.8	18	8	US-10-299-054A-7571	Sequence 7571, Ap
C 27	10.4	57.8	18	8	US-10-299-054A-11547	Sequence 11547, A
C 28	10.4	57.8	19	9	US-10-259-275-73	Sequence 73, Appl
C 29	10.4	57.8	19	9	US-10-358-037-4	Sequence 4, Appl
C 30	10.4	57.8	20	1	PCT-US02-40955-22	Sequence 88, Appl
C 31	10.4	57.8	20	8	US-10-274-586-88	Sequence 88, Appl
C 32	10.2	56.7	15	8	US-10-367-892-12063	Sequence 10363, A
C 33	10.2	56.7	15	8	US-10-367-892-12851	Sequence 12851, A
C 34	10.2	56.7	15	8	US-10-367-892-14893	Sequence 14893, A
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C 37	10.2	56.7	15	8	US-10-287-787-1488	Sequence 1488, Ap
C 38	10.2	56.7	15	8	US-10-287-787-6615	Sequence 6615, Ap
C 39	10.2	56.7	15	8	US-10-287-787-6616	Sequence 6616, Ap
C 40	10.2	56.7	15	8	US-10-287-787-19392	Sequence 19392, A
C 41	10.2	56.7	15	8	US-10-287-787-19393	Sequence 19393, A
C 42	10.2	56.7	16	8	US-10-367-892-6101	Sequence 6101, Ap
C 43	10.2	56.7	16	8	US-10-367-892-6102	Sequence 6102, Ap
C 44	10.2	56.7	16	8	US-10-299-054A-4121	Sequence 4121, Ap
C 45	10.2	56.7	16	8	US-10-299-054A-5693	Sequence 5693, Ap

## ALIGNMENTS

RESULT 1  
PCT-US03-04088-255  
Sequence 255, Application PCT/US0304088  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Mcswigen, James  
APPLICANT: Beigelman, Leonid  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene  
FILE REFERENCE: 02-708-A (400/080)  
CURRENT APPLICATION NUMBER: PCT/US03/04088  
CURRENT FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: US 60/396,600  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 255  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sens.  
OTHER INFORMATION: Region  
PCT-US03-04088-255

Query Match 65.6%, Score 11.8; DB 1; Length 19;  
Best Local Similarity 86.7%, Pred. No. 8.1e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
3 UGCCUACUGCGCG 17  
||||| ||| |||||

Db 5 UGCGCAUCCGUGCG 19

## RESULT 2

US-09-827-383B-1775/c  
; Sequence 1775, Application US/09827383B  
; GENERAL INFORMATION:  
; APPLICANT: Miltmann, Michael  
; APPLICANT: Morris, Macdonald  
; APPLICANT: Ryder, Thomas  
; APPLICANT: Lockhart, David  
; APPLICANT: Altimetrix, Inc.  
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays  
; FILE REFERENCE: 3108.1  
; CURRENT APPLICATION NUMBER: US/09/827,383B  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/195,585  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 1775  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-09-827-383B-1775

Query Match 65.6%; Score 11.8; DB 6; Length 20;  
Best Local Similarity 73.3%; Pred. No. 8.1e+03;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAUGCCUAGUGUG 15  
|||:||||:|:|:|  
Db 19 AAGGCGCTATGCGG 5

## RESULT 3

US-10-289-762-3336/c  
; Sequence 3336, Application US/10289762  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 3336  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-3336

Query Match 65.6%; Score 11.8; DB 8; Length 20;  
Best Local Similarity 66.7%; Pred. No. 8.1e+03;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAUGCCUAGUGUG 15  
|||:||||:|:|:|  
Db 20 AATGCGCTAATGATG 6

## RESULT 4

US-10-259-275-56  
; Sequence 56, Application US/10259275  
; GENERAL INFORMATION:  
; APPLICANT: Lemon, Stanley M.  
; APPLICANT: Yi, Minkyung  
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
; FILE REFERENCE: 265.0007 0120  
; CURRENT APPLICATION NUMBER: US/10/259,275

; CURRENT FILING DATE: 2003-01-13

; PRIOR APPLICATION NUMBER: US 60/171,909

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: US 09/747,419

; PRIOR FILING DATE: 2000-12-23

; PRIOR APPLICATION NUMBER: US 60/325,236

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US 60/338,123

; PRIOR FILING DATE: 2001-11-13

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 56

; LENGTH: 18

; TYPE: DNA

; ORGANISM: ARTIFICIAL

; FEATURE:  
; OTHER INFORMATION: primer  
US-10-259-275-56

Query Match 63.3%; Score 11.4; DB 9; Length 18;  
Best Local Similarity 69.2%; Pred. No. 1.4e+04;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAUGCCUAGUGUG 13  
|||:||||:|:|:|  
Db 5 AATGCGCTATGCG 17

## RESULT 5

US-10-367-892-16232  
; Sequence 16232, Application US/10367892  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Deionococcus radiodurans RI complete genome, Plasmid  
; FILE REFERENCE: Jim Zegeer Law Offices -703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/367,892  
; CURRENT FILING DATE: 2003-03-06  
; NUMBER OF SEQ ID NOS: 25502  
; SOFTWARE: Proprietary  
; SEQ ID NO 16232  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Deionococcus radiodurans RI complete genome, Plasmid  
; FEATURE:  
; LOCATION: (1951714)...(1951728)  
; OTHER INFORMATION: Chromosome - 1 Strand - positive ConnectonObjectNumber = 18  
US-10-367-892-16232

Query Match 60.0%; Score 10.8; DB 8; Length 15;  
Best Local Similarity 71.4%; Pred. No. 2.9e+04;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCUAGUGUGUG 17  
||||:||||:|:|:|  
Db 2 GCGCGGTGCGTGG 15

## RESULT 6

US-10-367-892-19783  
; Sequence 19783, Application US/10367892  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Deionococcus radiodurans RI complete genome, Plasmid  
; FILE REFERENCE: Jim Zegeer Law Offices -703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/367,892  
; CURRENT FILING DATE: 2003-03-06  
; NUMBER OF SEQ ID NOS: 25502  
; SOFTWARE: Proprietary  
; SEQ ID NO 19783  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Deionococcus radiodurans RI complete genome, Plasmid  
; FEATURE:

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; LOCATION: (2409107)...(2409121)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectorObjectNumber = 23195
US-10-367-892-19783
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 8; Length 15;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCUAGCGGCG 17
    ||| : |||: |||
    2 GGCCGTCGTCGCG 15

RESULT 7
US-10-303-778-1079
; Sequence 1079, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1079
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-1079
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 9; Length 15;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCUAGCGGCG 17
    |||:|:|:|:|
    2 GGCCATAGCGTCGCG 15

RESULT 8
US-10-287-787-23056
; Sequence 23056, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 23056
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (3325540)...(3325555)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 25456
US-10-287-787-23056
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 8; Length 16;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGGCCUAGCGGCG 16
    : |||:|:|:|
    2 TCGCCATCGCGCG 15

RESULT 9
US-10-287-787-23057/c
; Sequence 23057, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 23057
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (3325540)...(3325555)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectorObjectNumber = 25
US-10-287-787-23057
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 8; Length 16;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGGCCUAGCGGCG 16
    : |||:|:|:|
    15 TCGCCATCGCGCG 2

RESULT 10
PCT-US03-10154-33/c
; Sequence 33, Application PC/TUS0310154
; GENERAL INFORMATION:
; APPLICANT: XOMA TECHNOLOGY LTD.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; FILE REFERENCE: 13698W001
; CURRENT APPLICATION NUMBER: PCT/US03/10154
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homosapiens
; NAME/KEY: misc.feature
; FEATURE:
; OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers -Reverse Primer GR
; OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR
PCT-US03-10154-33
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 1; Length 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAUGGCCUAGCGU 14
    || |||| |:|||
    15 AAGGCCATCGCGT 2

RESULT 11
US-10-404-724-33/c
; Sequence 33, Application US/10404724
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
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RESULT 15
US-10-287-787-16018
: Sequence 16018, Application US/10287787
: GENERAL INFORMATION:
: APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
: TITLE OF INVENTION: Caulobacter crescentus complete genome
: FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
: CURRENT APPLICATION NUMBER: US/10/287,787
: CURRENT FILING DATE: 2003-03-03
: NUMBER OF SEQ ID NOS: 27958
: SOFTWARE: Proprietary
: SEQ ID NO 16018
: LENGTH: 19
: TYPE: DNA
: ORGANISM: Caulobacter crescentus complete genome.

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; FEATURE:
; LOCATION: (2427911)...(2427929)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectionObjectNumber = 17744
US-10-287-787-16018

Query Match          60.0%; Score 10.8; DB 8; Length 19;
Best Local Similarity 78.6%; Pred. No. 3e+04;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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   ||| :||| |||
Db 4 GCCCATCGCGCGCA 17

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Job time : 448.636 secs
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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

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Title: US-09-780-929-97

Perfect score: 15  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	15	100.0	15	US-09-780-929-97	Sequence 97, Appl
2	12	80.0	17	US-09-277-0268-1704	Sequence 1704, Ap
3	11.4	76.0	20	US-09-201-228A-3093	Sequence 3093, Ap
4	11.4	76.0	20	US-10-003-919-50	Sequence 50, Appl
5	11	73.3	19	US-60-216-745-13493	Sequence 13493, A
6	10.8	72.0	17	US-09-730-289B-606	Sequence 606, App
7	10.8	72.0	17	US-09-730-289B-607	Sequence 607, App
8	10.8	72.0	18	US-09-579-536-4	Sequence 607, App
9	10.8	72.0	18	US-09-579-536C-4	Sequence 4, Appl
10	10.8	72.0	18	US-09-688-078-12	Sequence 12, Appl
11	10.8	72.0	18	US-10-213-329-4	Sequence 4, Appl
12	10.8	72.0	18	US-60-216-745-5964	Sequence 4, Appl
13	10.8	72.0	20	PCR-US02-03159-72	Sequence 5064, Ap
14	10.8	72.0	20	US-09-068-506-50	Sequence 22, Appl
15	10.8	72.0	20	US-09-514-000-12603	Sequence 50, Appl
16	10.8	72.0	20	US-09-514-000-15028	Sequence 15028, A
17	10.8	72.0	20	US-09-703-708-12172	Sequence 12172, A
18	10.8	72.0	20	US-60-164-320-12172	Sequence 12172, A
19	10.8	72.0	20	US-60-183-791-12172	Sequence 12172, A
20	10.4	69.3	12	PCR-US98-26935-217	Sequence 217, App
21	10.4	69.3	12	US-09-215-436-217	Sequence 217, App

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22 10.4 69.3 12 22 US-09-581-970A-217 Sequence 217, App
23 10.4 69.3 17 21 US-09-546-745A-5653 Sequence 5653, Ap
24 10.4 69.3 17 30 US-09-792-818-40 Sequence 40, Appl
25 10.4 69.3 17 30 US-09-792-818-41 Sequence 41, Appl
26 10.4 69.3 17 30 US-09-792-818-222 Sequence 222, Appl
27 10.4 69.3 17 30 US-09-792-818-223 Sequence 223, Appl
28 10.4 69.3 17 30 US-09-792-818-562 Sequence 562, App
29 10.4 69.3 17 64 US-60-201-255-24 Sequence 24, Appl
30 10.4 69.3 19 36 US-09-969-373-2697 Sequence 2697, Ap
31 10.2 68.0 15 1 PCT-US02-25942-54 Sequence 54, Appl
32 10.2 68.0 15 1 PCT-US02-25942-55 Sequence 55, Appl
33 10.2 68.0 15 1 PCT-US02-25942-56 Sequence 56, Appl
34 10.2 68.0 15 1 PCT-US02-25942-57 Sequence 57, Appl
35 10.2 68.0 15 11 US-08-774-306-447 Sequence 447, App
36 10.2 68.0 15 16 US-09-274-553-1004 Sequence 1004, Ap
37 10.2 68.0 15 16 US-09-274-553B-469 Sequence 469, App
38 10.2 68.0 15 16 US-09-274-553C-469 Sequence 469, App
39 10.2 68.0 15 16 US-09-274-553D-469 Sequence 469, App
40 10.2 68.0 15 19 US-09-504-231A-469 Sequence 469, App
41 10.2 68.0 15 19 US-09-504-231B-469 Sequence 469, App
42 10.2 68.0 15 23 US-09-611-931-469 Sequence 469, App
43 10.2 68.0 15 23 US-09-611-931A-469 Sequence 469, App
44 10.2 68.0 15 24 US-09-633-515-447 Sequence 447, App
45 10.2 68.0 15 42 US-10-227-567-54 Sequence 54, Appl
```

## ALIGNMENTS

## RESULT 1

US-09-780-929-97

Sequence 97, Application US/09780929

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: Breaker, Ronald

APPLICANT: Beigelman, Leo

TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity

FILE REFERENCE: MBH80-884-H (560/901) 929

CURRENT FILING DATE: US/09/780, 929

PRIOR APPLICATION NUMBER: 2001-02-08

PRIOR FILING DATE: 2000-02-08

NUMBER OF SEQ ID NOS: 126

SOFTWARE: Patent version 3.0

SEQ ID NO 97

LENGTH: 15

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-780-929-97

Query Match 100.0%; Score 15; DB 30; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGUAAACGUGAAGAU 15

Db 1 AGUAAACGUGAAGAU 15

## RESULT 2

US-09-277-026B-1704

Sequence 1704, Application US/09277026B

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela

APPLICANT: Roberts, Elisabeth

APPLICANT: Jarvis, Thale

APPLICANT: Coesholt, Claire

TITLE OF INVENTION: Method and Reagents for the Treatment of Diseases or Conditions R

FILE REFERENCE: MBH80-824-A (239/121)

```
CURRENT APPLICATION NUMBER: US/09/277, 026B
CURRENT FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/079, 678
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 6652
SOFTWARE: Patent version 3.0
SEQ ID NO 1704
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: Oligonucleotide substrate
US-09-277-026B-1704
Query Match 80.0%; Score 12; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 AGUAAACGUGA 12

Db 5 AGUAAACGUGA 16

## RESULT 3

US-09-201-228A-3093

Sequence 3093, Application US/09201228A

GENERAL INFORMATION:

APPLICANT: Griffiths, Remy

APPLICANT: Holseth, Susan K.

APPLICANT: Zagursky, Robert John

APPLICANT: Metcalf, Benjamin J.

APPLICANT: Peek, Joel A.

APPLICANT: Sankaran, Banumathi

APPLICANT: Fletcher, Leah Diane

TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF

TITLE OF INVENTION: INFECTION

FILE REFERENCE: 9710-0004-999

CURRENT APPLICATION NUMBER: US/09/201, 228A

CURRENT FILING DATE: 1998-11-30

PRIOR APPLICATION NUMBER: US 60/107, 077

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: FR 97-16034

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: FR 97-15041

PRIOR FILING DATE: 1997-11-28

NUMBER OF SEQ ID NOS: 5981

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3093

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer

US-09-201-228A-3093

Query Match 76.0%; Score 11.4; DB 16; Length 20;

Best Local Similarity 69.2%; Pred. No. 4.7e+04;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 AUAACGUGAAGAU 15

Db 2 ATAACGTGAGAT 14

## RESULT 4

US-10-003-919-50/C

Sequence 50, Application US/10003919

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

Query Match	72.0%	Score 10.8	DB 22	Length 18
Best Local Similarity	71.4%	Pred. No. 1e+05		
Matches 10; Conservative	2;	Mismatches 2;	Indels 0;	Gaps 0;
OY 2 GATACCGGAGGAT 15				
DB 1 GAGACCGTGAAGAT 14				

Query Match	72.0%	Score 10.8;	DB 42;	Length 18;
Best Local Similarity	71.4%	Pred. No.1e+05;		
Matches	10;	Conservative	2;	Mismatches
				Indels
				Gaps
Qy	2 GAUACGCGAGACU	15		
Db	1 GAGACCGTGAAGAT	14		

```

RESULT 12
US-60-216-745-5964
, Sequence 5964, Application US/60216745
, GENERAL INFORMATION:
, APPLICANT: Cohen, Daniel
, APPLICANT: Blumenfeld, Marla
, APPLICANT: Chumakov, Ilya
, APPLICANT: Abderrahim, Hadi
, APPLICANT: Dufauré-Gare, Isabelle
, TITLE OF INVENTION: BIOMOLETIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY
, FILE REFERENCE: 84.051.PRO
, CURRENT APPLICATION NUMBER: US/60/216, 745
, CURRENT FILING DATE: 2000-06-30
, NUMBER OF SEQ. ID NOS: 13665
, SOFTWARE: Patent.pm
, SEQ. ID NO 5964
, LENGTH: 18
, TYPE: DNA
, ORGANISM: Homo Sapiens
, FEATURE:
, NAME/KEY: primer_bind
, LOCATION: 1..18
, OTHER INFORMATION: upstream amplification primer 99-25537 for SEQ. 1433,
US-60-216-745-5964

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; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
; FILE REFERENCE: RTS-0256
; CURRENT APPLICATION NUMBER: US/10/003,919
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-003-919-50

Query Match
Best Local Similarity 76.0%; Score 11.4; DB 38; Length 20;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAUACGUGAAGA 14
DB 20 GACACGCGAAGA 8

RESULT 5
US-60-216-745-13493
; Sequence 13493, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaire-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
; FILE REFERENCE: 84, US1, PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent, pm
; SEQ ID NO 13493
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-50547 for SEQ 4431, in complet
US-60-216-745-13493

Query Match
Best Local Similarity 73.3%; Score 11; DB 65; Length 19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 UACGUGAAGA 14
DB 3 TAACGTGAGA 13

RESULT 6
US-09-730-289B-606/C
; Sequence 606, Application US/09730289B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 606

; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-606

Query Match
Best Local Similarity 72.0%; Score 10.8; DB 29; Length 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUACGUGAAGA 14
DB 17 AGATACATGAGA 4

RESULT 7
US-09-730-289B-607/C
; Sequence 607, Application US/09730289B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 607
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-607

Query Match
Best Local Similarity 72.0%; Score 10.8; DB 29; Length 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUACGUGAAGA 14
DB 15 AGATATGTGAGA 2

RESULT 8
US-09-579-536-4
; Sequence 4, Application US/09579536
; GENERAL INFORMATION:
; APPLICANT: MACIAG, Thomas
; APPLICANT: ZIMRIN, Ann B.
; APPLICANT: SMALL, Deena J.
; APPLICANT: PRIDOVSKY, Igor A.
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
; FILE REFERENCE: 36-102 (200036,0010) Maciag et al.
; CURRENT APPLICATION NUMBER: US/09/579,536
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/199,865
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US97/09407
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/018,841
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
US-09-579-536-4
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